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Minimum DB
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Listing first 45 summaries
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       Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed.
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1 US-08-243-545-6
2 US-08-93-962-6
3 US-09-100-100-1
3 US-09-109-100-1
5 PCT-US94-05365-6
5 US-09-109-100-1
6 US-09-109-100-1
7 US-08-220-379B-7
7 US-08-230-386-2
7 US-08-230-379B-7
7 US-08-317-523A-9
7 US-08-317-523A-9
7 US-08-751-965-9
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## ALIGNMENTS

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RESULT 1
US-08-243-545-6
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                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/162,407
FILING DATE: 03-DEC-1993
APPLICATION NUMBER: 08/111,758
FILING DATE: August 25, 1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                               APPLICATION NUMBER: 08/106,463
FILING DATE: August 12, 1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/068,394
FILING DATE: May 24, 1993
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: Apple Macintosh 7.0.1
OPERATING SYSTEM: Macintosh 7.0.1
SOFTWARE: Microsoft Word, Version
CURRENT APPLICATION DATA: US/08/243,545
FILING NATE: 11-MAX-1994
CLASSIFICATION: 435
                                                            TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
TELEFAX: (206) 233-0644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Lyman, Stewart D. APPLICANT: Beckmann, M. Patricia TITLE OF INVENTION: Ligands for INUMBER OF SEQUENCES: 8
                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: Malaska, Stephen L.
REGISTRATION NUMBER: 32,6
                               TELEFAX: (2011)
TELEFAX: 756822
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CITY: Seattle
STATE: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
                                                                                                                                 REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE:
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                                                                                                                                   32,655
ER: 281
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Best Local Similarity
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MEDIUM TYPE: Floppy disk

COMPUTER: Apple Macintosh

OPERATING SYSTEM: Macintosh 7.0.1

SOFTWARE: Microsoft Word, Version #:

CURRENT APPLICATION NUMBER: US/08/993,962
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                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 424
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US/08/162,407
                                                  REFERENCE/DOCKET NUMBER: 2813-C TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/106,4
FILING DATE: August 12, 1993
                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: Malaska, Stephen L.
REGISTRATION NUMBER: 32,6
                                                                                                                                                        CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: May 24,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Lyman, Stewart D.
APPLICANT: Beckmann, M. Patricia
TITLE OF INVENTION: Ligands for flt3/flk-2 Receptors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/08/162,4
FILING DATE: December 3, 1993
APPLICATION NUMBER: 08/111,758
FILING DATE: August 25, 1993
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     181
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OLECULE TYPE: protein
                 TELEFAX:
                                TELEPHONE:
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51 University Street
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                                 (206) 587-0430
                                                                                                                                                    May 24,
                                                                                                                                                                                                                                                                                                                                                                                              UMBER: US/08/993,962
December 18, 1997
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RESULT 3
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Patent No.
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Best Local
                                                                                                                    APPLICATION NUMBER: 08/111,758
FILING DATE: August 25, 1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/106,463
FILING DATB: August 12, 1993
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION MUMBER: 08/068,394
FILING DATE: May 24, 1993
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                                                                  APPLICATION NUMBER: 08/06
FILING DATE: May 24, 1993
ATTORNEY/AGENT INFORMATION:
NAME: Malaska, Stephen L.
REGISTRATION NUMBER: 32,6
                                                                                                                                                                                                                                                                 CLASSIFICATION DATA:
PRIOR APPLICATION UMBER: US/08/162,407
                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Microsoft Word, Version CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Lyman, Stewart D. APPLICANT: Beckmann, M. Patricia TITLE OF INVENTION: Ligands for
                                REFERENCE/DOCKET NUMBER: 28
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: Stephen L.
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TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk COMPUTER: Apple Macintosh OPERATING SYSTEM: Macintos
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                                                                                                                                                                                                                                          FILING DATE: December:
                                                                                                                                                                                                                                                                                                            CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                               FILING DATE:
                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/09/160,841
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o. 6190655
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                (206) 587-0430
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                          RESULT 5
PCT-US94-05365-6
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Best Local S
Matches 235
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CURRENT FILING DATE: 1998-07-02
NUMBER OF SEQ ID NOS: 20
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 1
LENGTH: 235
TYPE: PRT
ORGANISM: Homo sapiens
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Sequence 6, Application PC/TUS9405365 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Graddis, Thomas J.
APPLICANT: McGrew, Jeffrey T.
TITLE OF INVENTION: FLT3-I MUTANTS AND METHODS OF
FILE REFERENCE: 03260.0028
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SEQUENCE CHARACTERISTICS:
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mino acid
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Pred. No. 1.7e-117;
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Best Local S
Matches 235
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COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-TOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION UMBER: PCT/US94/05365
FILING DATE: May 24, 1994
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APPLICATION NUMBER:
FILING DATE: May 11,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Lyman, Stewart D.
APPLICANT: Beckmann, M. Patricia
TITLE OF INVENTION: Ligands for flt3/flk-2 Receptors
                                                                                                                                                                                                                                                          MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                REGISTRATION NUMBER: 32,655
REFERENCE/DOCKET NUMBER: 28
TELECOMMUNICATION INFORMATION:
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APPLICATION NUMBER:
FILING DATE: August
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APPLICATION NUMBER: 08/162,407
FILING DATE: December 3, 1993
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APPLICATION NUMBER:
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CORRESPONDENCE ADDRESS:
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ATTORNEY/AGENT INFORMATION:
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APPLICATION NUMBER:
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CITY: Seattle
STATE: Washing
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TELEFAX: 756822
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                                   61
                                                                                                                                                                       Local Similarity
nes 235; Conserv
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RFVQTNISRLLQETSEQLVALKPWITRQNFSRCLELQCQPDSSTLPPPWSPRPLEATAPT 180
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August 25, 1993
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                                                                                                                                                                      100.0%; Score 1242; DB 5; 100.0%; Pred. No. 1.7e-117; tive 0; Mismatches 0;
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, 1994
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US-09-109-100-18
                 QΥ
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SEQ ID NO 10
LENGTH: 212
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                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: Graddis, Thomas J.
APPLICANT: MCGrew, Jeffrey T.
TITLE OF INVENTION: FLT3-L MUTANTS AND METHODS
FILE REFERENCE: 03260.0028
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Best Local
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CURRENT FILING DATE: 1998-07-02
NUMBER OF SEQ ID NOS: 20
SOFTWARE: PatentIn Ver: 2.1
SEQ ID NO 18
LENGTH: 209
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                                                   Matches
                                                                   Query Match
Best Local :
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APPLICANT: McGrew, Jeffrey T.
TITLE OF INVENTION: FLT3-L MUTANTS AND METHODS
FILE REFERENCE: 03260.0028
                                                                                                                     ORGANISM: Homo sapiens -09-109-100-18
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27 TQDCSFQHSPISSDFAVKIRELSDYLLQDYPVTVASNLQDEELCGGLWRLVLAQRWMERL 86
                                                  Match 89.7%;
Local Similarity 100.0%;
les 209; Conservative
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                                                                   Score 1114; DB 4;
Pred. No. 1.2e-104;
                                                     Mismatches
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GENERAL INFORMATION:
APPLICANT: Graddis, Thomas J.
APPLICANT: McGrew, Jeffrey T.
APPLICANT: McGrew, Jeffrey T.
TITLE OF INVENTION: FLT3-L MUTANTS AND METHODS OF
FILE REFERENCE: 03260.0028
CURRENT APPLICATION NUMBER: US/09/109,100C
CURRENT FILING DATE: 1998-07-02
NUMBER OF SEQ ID NOS: 20
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 12
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; ORGANISM: Homo sapiens US-09-109-100-12
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APPLICANT: Graddis, Thomas J.
APPLICANT: McGrew, Jeffrey T.
APPLICANT: MCGrew, Jeffrey T.
TITLE OF INVENTION: FLT3-L MUTANTS AND METHODS
FILE REFERENCE: 03260.0028
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CURRENT FILING DATE: 1998-07-02
NUMBER OF SEQ ID NOS: 20
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 20
TYPE: PRT
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                               TYPE: PRT
                                           LENGTH: 209
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APPLICANT: Graddis, Thomas J.
APPLICANT: McGrew, Jeffrey T.
FITTLE OF INVENTION: FLT3-L MUTANTS AND METHODS OF
FILE REFERENCE: 03260.0028
CURRENT APPLICATION NUMBER: US/09/109,100C
CURRENT FILING DATE: 1998-07-02
NUMBER OF SEQ ID NOS: 20
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 14
LENGTH: 209
TYPE: PRT
GENERAL INFORMATION:

APPLICANT: Graddis, Thomas J.

APPLICANT: McGrew, Jeffrey T.

TITLE OF INVENTION: FLT3-L MUTANTS AND METHODS

FILE REFERENCE: 03260.0028

CURRENT APPLICATION NUMBER: US/09/109,100C

CURRENT FILING DATE: 1998-07-02
                                                                                                  US-09-109-100-17; Sequence 17, Application US/091091000; Patent No. 6291661
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; Patent No. 6291661
; GENERAL INFORMATION:
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Best Local Similarity
Matches 208; Conserv
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Pred. No. 3e-104;
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APPLICANT: Graddis, Thomas J.
APPLICANT: MCGrew, Jeffrey T.
TITLE OF INVENTION: FLT3-L MUTANTS AND METHODS OF
FILE REFERENCE: 03260.0028
CURRENT APPLICATION NUMBER: US/09/109/100C
CURRENT FILING DATE: 1998-07-02
NUMBER OF SEQ ID NOS: 20
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 11
LENGTH: 209
TYPE: PRT
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; TYPE: PRT
; ORGANISM: HOMO S
US-09-109-100-17
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US-09-109-100-11
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SOFTWARE: PatentIn Ver
SEQ ID NO 17
LENGTH: 209
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Best Local
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Best Local :
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                                                                                                                                                                  61 KTVAGSKMQGLLERVNTEIHFVTKCAFQPPPSCLRFVQTNISRLLQETSEQLVALKPWIT 120
                                                                                                                                                                                                                                                                                      Match 89.2%;
Local Similarity 99.5%;
                                                                                                                                                                                KTVAGSKMQGLLERVNTEIHFVTKCAFQPPPSCLRFVQTNISRLLQETSEQLVALKPWIT 146
                                                      WQRTRRRTPRPGEQVPPVPSPQDLLLVEH
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Pred. No. 4.8e-104;
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Pred. No. 3e-104;
1; Mismatches
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Sequence 15, Application Patent No. 6291661

US/09109100C

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APPLICANT: Graddis, Thomas J.
APPLICANT: McGrew, Jeffrey T.
TITLE OF INVENTION: FLT3-L MUTANTS AND METHODS OF USE
FILE REFERENCE: 03260.0028
CUBRENT APPLICATION NUMBER: US/09/109,100C
CUBRENT FILING DATE: 1998-07-02
NUMBER OF SEQ ID NOS: 20
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 15
LENGTH: 209
TYPE: PRT
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US-09-109-100-13
; Sequence 13, Application US/09109100C
patent No. 6291661
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-109-100-13
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Best Local Similarity
Matches 208; Conserval
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Best Local Similarity 99.5%;
Matches 208; Conservative
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CURRENT FILING DATE: 1998-07-02
NUMBER OF SEQ ID NOS: 20
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Graddis, Thomas J.
APPLICANT: McGrew, Jeffrey T.
TITLE OF INVENTION: FLT3-L MUTANTS AND METHODS OF USE
FILE REFERENCE: 03260.0028
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                                KTVAGSKMQGLLERVNTEIHFVTKCAFQPPPSCLRFVQTNISRLLQETSEQLVALKPWIT 120
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                                                                 RQNFSRCLELQCQPDSSTLPPPWSPRPLEATAPTAPQPPLLLLLLLLPVGLLLLAAAWCLH 206
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Pred. No. 6e-104;
0; Mismatches 1;
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Pred. No. 4.8e-104;
0; Mismatches 1; Indels
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; SEQ ID NO 8
LENGTH: 209
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-109-100-8
Search completed: November 24, 2002, 10:12:44 Job time: 15.1116 secs
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US-09-109-100-8
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Best Local Simi
Matches 208;
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CURRENT FILING DATE: 1998-07-02
NUMBER OF SEQ ID NOS: 20
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Graddis, Thomas J.
APPLICANT: McGrew, Jeffrey T.
TITLE OF INVENTION: FLT3-L MUTANTS AND METHODS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILE REFERENCE: 03260.0028
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                                                                        WQRTRRRTPRPGEQVPPVPSPQDLLLVEH 235
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                                                                                                                                                                           KTVAGSKMQGLLERVNTEIHFVTKCAFQPPPSCLRFVQTNISRLLQETSEQLVALKPWIT 120
                                                          WQRTRRRTPRPGEQVPPVPSPQDLLLVEH
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Database :
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq
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Perfect score:
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length: 2000000000
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1544.781 Million cell updates/sec
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	11	10	9	8							р-1	Result No.	
78.5	78.5	78.5	79	79.5	79.5	80	80.5	80.5	80.5	81	82.5	82.5	83.5	83.5	83.5	84	84.5	85	86	87	88	95.5	594.5	61,6.5	768.5	879	879	1223	Score	
6.4	6.4	٠			٠		6.6			٠	6.7	٠		6.8		٠		٠	7.0	7.1	7.2	7.	48.6	G	6	71.9	7	100.0	Query Match 1	
379	315	122	1101	745	399	382	395	394	391	4131	431	378	2476	552	552	1409	939	181	962	291	843	909	178	245	235	220	220	231	Length	
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77	77.5	77.5	77.5	77.5	77.5	77.5	77.5	78	78	78	78	78	78	78.5	78.5
6.3	6. <sub>3</sub>	6.3	6.3	6.3	6.3	6.3	6.3	6.4	6.4	6.4	6.4	6.4	6.4	6.4	6.4
619	811	774	774	746	579	456	266	1715	1601	908	806	743	224	3068	468
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D86509	E72003	H81540	B86492	S67203	JC7629	в72130	A45844	T06145	AE2011	S51293	E64221	T34632	I37243	A44062	T23091
S/T protein kinase	hypothetical prote	hypothetical prote	hypothetical prote	probable membrane	membrane-type friz	frame-shift with c	MHC class II histo	disease resistance	hypothetical prote	probable membrane	phenylalanine-tRNA	probable bi-functi	CMRF-35 antigen -	genome polyprotein	hypothetical prote

## ALIGNMENTS

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flt3/flk-2 ligand precursor mouse
c;Species: Mus musculus (house mouse)
c;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 08-Oct-1999
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 08-Oct-1999
C;Accession: A49265; I49347; I49346; S43290
R;Lyman, S.D.; James, L.; Vanden Bos, T.; de Vries, P.; Brasel, K.; Gliniak, B.; Holl D.; Williams, D.E.; Beckmann, M.P.
Cell 75, 1157-1167, 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: DNA, A; Rosidues: 1-197, L1, 198-231 < RE2>
A; Residues: 1-197, L1, 198-231 < RE2>
A; Coss-references: EMBL:U29875; NID:g1072039; PIDN:AAA90951.1; PID:g1072040
A; Cross-references: EMBL:U29875; NID:g1072039; PIDN:AAA90951.1; PID:g1072040
A; C: Culpepper, J.; Campbell, D.; McClanahan, T.; Zurawski, S.; Bazan, J.F.; felt, A.; Muench, M.; Kelner, G.; Namikawa, R.; Rennick, D.; Roncarolo, M.G.; Zlotnik Nature 368, 643-648, 1994
A; Title: Ligand for FLT3/FLK2 receptor tyrosine kinase regulates growth of haematopoi A; Reference number: S43290; MUID:94195428; PMID:8145851
A; Accession: S43290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: GB:L23636; NID:g439441; PIDN:AAA39436.1; PID:g439442 R;Lyman, S.D.; Stocking, K.; Davison, B.; Fletcher, F.; Johnson, L.; Escol Oncogene 11, 1165-1172, 1995 A;Title: Structural analysis of human and murine flt3 ligand genomic loci A;Reference number: 139075; MUID:96032581; PMID:7566977
DЬ
                                                                                                                                                                                                                                                                       C;Genetics:
A;Introns: 11/3; 49/3; 67/3; 115/3; 164/1; 224/3
C;Keywords: transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: mRNA
A; Residues: 1-197, 'L', 198-231 <HAN>
A; Experimental source: clone T110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Title: Molecular cloning of a ligand for the flt3/flk-2 tyrosine kinase receptor: a A;Reference number: A49265; MUID:94084791; PMID:7505204 A;Accession: A49265
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A;Molecule type: DNA
A;Residues: 1-163,'G',165,'HYAG' <RES>
A;Residues: 1-163,'G',165,'HYAG' <RES>
A;Cross-references: EMBL:029875; NID:g1072039; PIDN:AAA90952.1; PID:g1072041
A;Accession: I49346
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Status: preliminary
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                                                                                                                                                                      Query Match
Best Local
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                                1 MTVLAPAWSPNSSLLLLLLLLLSPCLRGTPDCYFSHSPISSNFKVKFRELTDHLLKDYPVT 60
MTVLAPAWSPNSSLLLLLLLLSPCLRGTPDCYFSHSPISSNFKVKFRELTDHLLKDYPVT 60
                                                                                                                                     Conservative
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                                                                                                                                                                  Score 1223; DB 2;
Pred. No. 2.9e-101;
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A;Title: Identification of soluble and membrane-bound isoforms of the murine A;Reference number: 158343; MUID:95124710; PMID:7824267
A;Accession: I58343
                                                        Qy
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A;Molecule type: mRNA
A;Residues: 1-220 <RES>
A;Cross-references: GB:S76459; NID:g913479; PIDN:AAB33069.1; PID:g913480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Species: Mus sp. (mouse)
C;Date: 26-Jul-1996 #sequence_revision
C;Accession: I58343
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A;Status: preliminary A;Molecule type: mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            flt3 ligand isoform 5H - mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    neit, A.; Muench, M.; Kel
Nature 368, 643-648, 1994
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:Residues: 1-220 <HAN>
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1 MTVLAPAWSPNSSLLLLLLLLSPCLRGTPDCYFSHSPISSNFKVKFRELTDHLLKDYPVT
                                                                                                                      Local Similarity
nes 177; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LRFVQTNISHLLKDTCTQLLALKPCIGKACQNFSRCLEVQCQPDSSTLLPPRS----PIA 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VAVNLQDEKHCKALWSLFLAQRWIEQLKTVAGSKMQTLLEDVNTEIHFVTSCTFQPLPEC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MTVLAPAWSPNSSLLLLLLLLSPCLRGTPDCYFSHSPISSNFKVKFRELTDHLLKDYPVT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VAVNLQDEKHCKALWSLFLAQRWIEQLKTVAGSKMQTLLEDVNTEIHFVTSCTFQPLPEC
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                                                                                                                          Conservative
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                                                                                                                                               71.9%;
82.3%;
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82.3%;
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                                                                                                                                            Score 879; DB 2
Pred. No. 1e-70;
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Pred. No. 1e-70;
                                                                                                                   Mismatches
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                                                                                                                                                                            DB 2;
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                                                                                                                      21;
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I38440
flt3 ligand
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C; Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 01-Dec-2000
C; Accession: I38440; I39075; S43292
R; Lyman, S.D.; James, L.; Johnson, L.; Brasel, K.; de Vries, P.; Escobar, S Blood 83, 2795-2801, 1994
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A;Molecule type: DNA
A;Residues: 1-235 <RE2>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-71,'A',73-235 <HAN>
A;Cross-references: GB:U04806; NID:g483844; PIDN:AAA17999.1; PID:g483845
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A; Residues: 1-235 < RES>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches 163;
                                                        178
                                                                                                                   181
                                                                                                                                                                               120
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                                                                                       ELPEPRPRQLLLLLLLLPLTLVLLAAAWGLRWQRARRR----GELHPGVPLP 228
                                                                                                                                                                                                                                                                                                                                  VAVNLQDEKHCKALWSLFLAQRWIEQLKTVAGSKMQTLLEDVNTEIHFVTSCTFQPLPEC
                                                                                                                                                                                                              LREVQTNISHLLKDTCTQLLALKPCIGKACQNESRCLEVQCQPDSSTLLPPRSPIALEAT 180
                                                                                                                                                                                                                                                                                                                                                                                                                   VASNLQDEELCGGLWRLVLAQRWMERLKTVAGSKMQGLLERVNTEIHFVTKCAFQPPPSC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LRFVQTNISHLLKDTCTQLLALKPCIGKACQNFSRCLEVQCQPDSSTLLPPRS----PIA 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VAVNLQDEKHCKALWSLFLAQRWIEQLKTVAGSKWQTLLEDVNTEIHFVTSCTFQPLPEC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VAVNLQDEKHCKALWSLFLAQRWIEQLKTVAGSKMQTLLEDVNTEIHFVTSCTFQPLPEC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   {\tt MTVLAPAWSPNSSLLLLLLLSPCLRGTPDCYFSHSPISSNFKVKFRELTDHLLKDYPVT}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LEATELPEPRPRQULLL-----LLLLPLTLVLLAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11/3; 48/3; 66/3; 114/3; 161/1; 220/3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          62.8%; Score 768.5; DB 2; 70.3%; Pred. No. 7.1e-61; tive 17; Mismatches 43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             codon AGT for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   the murine flt3
PMID:8180375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          K.; de Vries, P.; Escobar, S.S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         residue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
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ligand: a growth factor fo

Downe

Escobar,

25 as

9,

Gaps

4

120 59

177

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C:Species: Homo sapiens (man)
C:Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 21-Jul-2000
C:Accession: I39076
R:Lyman, S.D.; Stocking, K.; Davison, B.; Fletcher, F.; Johnson, L.; Escobar Oncogene 11, 1165-1172, 1995
A:Title: Structural analysis of human and murine flt3 ligand genomic loci.
A:Reference number: I39075; MUID:96032581; PMID:7566977
A:Accession: I39076
A:Status: preliminary; translated from GB/EMBL/DDBJ
                                     Qy
                                                                                                            Qy
                                                                                                                                                                                                                            C;Genetics:
A;Introns: 11/3; 48/3;
                                                                                                                                                                                                                                                                                    A;Status: preliminary; translated from GB/EMBL/DDBJA;Molecule type: DNAA;Residues: 1-178 <RES>
     밁
                                                                            DЬ
                                                                                                                                                                                                                                                            A;Cross-references: EMBL:U29874; NID:g1072036; PIDN:AAA90950.1; PID:g1072038
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Flt3 ligand alternatively spliced isoform - human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Qy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Molecule type: mRNA
A;Residues: 1-245 <HAN>
A;Note: the authors translated the codon AGT for residue 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Title: Ligand for FLT3/FLK2 receptor tyrosine kinase regulates growth of haematopoiet: A;Reference number: $43290; MUID:94195428; PMID:8145851 A;Accession: $43293 A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R; Hannum, C.; Culpepper, J.; Campbell, D.; McClanahan, T.; Zurawski, S.; Bazan, J.F.; felt, A.; Muench, M.; Kelner, G.; Namikawa, R.; Rennick, D.; Roncarolo, M.G.; Zlotnik, Nature 368, 643-648, 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Species: Homo sapiens (man)
C;Date: 20-Oct-1994 #sequence_revision 10-Nov-1995 #text_change 17-Mar-1999
C;Accession: S43293
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                                                                                                                                                   Query Match
Best Local S
Matches 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               219
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                                                                                                                                                                       Local Similarity
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                   VAVNLQDEKHCKALWSLFLAQRWIEQLKTVAGSKMQTLLEDVNTEIHFVTSCTFQPLPEC 120
                                                                                          MTVLAPAWSPNSSLLLLLLLLLSPCLRGTPDCYFSHSPISSNFKVKFRELTDHLLKDYPVT 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LRFVQTNISHLLKDTCTQLLALKPCIGKACQNFSRCLEVQCQPDSSTLLPPRSPIALEAT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MTVLAPAWSPNSSLLLLLLLLSPCLRGTPDCYFSHSPISSNFKVKFRELTDHLLKDYPVT 60
                                                                      IPSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PSHP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VAVNLQDEKHCKALWSLFLAQRWIEQLKTVAGSKMQTLLEDVNTEIHFVTSCTFQPLPEC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MTVLAPAWSP-TTYLLLLLLLLSSGLMGTQDCSFQHSPISSDFAVKIRELSDYLLQDYPVT 59
VASNLQDEELCGGLWRLVLAQRWMERLKTVAGSKMQGLLERVNTEIHFVTKCAFQPPPSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TWPRPHPGEDTEAHRGESPARGCI - - -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ELPEPRP----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VASNIQDEELCGALWRLVLAQRWMERLKTVAGSKMQGLLERVNTEIHFVTKCAFQPPPSC 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   231
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                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                              66/3; 114/3; 161/1
                                                                                                                                                                     48.6%;
73.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            50.4%; Score 616.5; DB 2 57.0%; Pred. No. 2.4e-47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RQLLLLLLLPLTLVLLAAAWGLRWQRARRRGELHPGVPL 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16;
                                                                                                                                                     14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      human
                                                                                                                                               Score 594.5; |
Pred. No. 1.5e
L4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                               1.5e-45;
ches 26;
                                                                                                                                                                                     DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            54;
                                                                                                                                                 Indels
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                                                                                                                                               Gaps
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                                                                        59
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A;Note: F20B18.200
C;Superfamily: disease resistance protein RPS2; leucine-rich alpha-2-glycoprotein rep
C;Keywords: leucine zipper; membrane protein; nucleotide binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C:Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 20-Apr-2000
C;Accession: A54809; A54811; T04264
R;Mindrinos, M.; Katagiri, F.; Yu, G.L.; Ausubel, F.M.
Cell 78, 1089-1099, 1994
                                                                                                                                  Ωy
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                                                                                                                                                                                                                                                                           Вр
                                                                                                                                                                                                                                                                                                                       Qγ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cell 78, 1089-1099, 1994
A;Title: The Arabidopsis thaliana disease resistance gene A;Reference number: A54809; MUID:95007758; PMID:7923358
В
                                      QΥ
                                                                                         В
                                                                                                                                                                                                                                                                                                                                                                       В
                                                                                                                                                                                                                                                                                                                                                                                                                δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Experimental source: cultivar Columbia; C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Status: preliminary; not
A;Molecule type: DNA; mRNA
A;Residues: 1-909 <BEN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Title: RPS2 of Arabidopsis thaliana: a leucine-rich repeat class of plant disease r A;Reference number: A54811; MUID:94377978; PMID:8091210 A;Accession: A54811
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: GB:U12860; NID:g549978; PIDN:AAA50236.1; PID:g549979 R;Bent, A.F.; Kunkel, B.N.; Dahlbeck, D.; Brown, K.L.; Schmidt, R.; Giray Science 265, 1856-1860, 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            disease resistance protein RPS2 - Arabidopsis thaliana N; Alternate names: protein F20B18.200 \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             밁
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Map position: 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Cross-references: EMBL: AL049483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: DNA
A; Residues: 1-909 <BEV>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Residues: 1-909 <MIN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: mRNA
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Best Local
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                                         209 G
763
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                                                                                                                               149 ACQNFSRCLEVQCQPDSSTLLPPRSPIALEATELPEPRPRQLLLLLLLLLLLLLLLAAAW 208
                                                                                                                                                                                                                                                                           595 VLPQELGNLRKLKHLDLQRTQFLQTIPRDAICWLSKLEVLNLYYSYAGWELQSFGEDEAE
                                                                                                                                                                                                                                                                                                                            63
                                                                                                                                                                                                                                                                                                                                                                                                              14 LILLLLLSPCLRGTPDCYFSHSPISSNFKVKFRELTD-----HLLKDYPVTVA-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
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G.
                                                                                      HGRNLRR-LSIKSCHDLEYLV---TPADFENDWLPS---LEVLTLHSLHNLTRV-----W
                                                                                                                                                                                                                           EIHF ------VTSCTFQPLPECLRF -- VQTNISHLLKDTCTQLLALK -PCIGK 148
                                                                                                                                                                                                                                                                                                                                                                     LTTLMLQQNSSLKKIPTGFFMHMPVLRVLDLSFTSITEIPLSIKYLVELYHLSMSGTKIS
                                                                                                                                                                                ELGFADLEYLENLTTLGITVLSLETLKTLFEFGALHKHIQHLHVEECNELLYFNLPSLTN 714
                                                                                                                                                                                                                                                                                                                    -----VNLQDEKHCKALWSLFL-----AQRWIEQLKTV-----AGSKMQTLLEDVNT 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LRFVQTNISRLLQETSEQLVALKPWITR--QNFSRCLELQCQP
                                           209
763
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
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22.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       compared with conceptual translation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 95.5;
Pred. No. 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; 68
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   163
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                                                                                      762
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RESULT T01438

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hypothetical protein GS034D21.1 - human (fragment)

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C; Geneti
A; Gene:
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R;Parkhill, J:; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B. deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.; il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell, Nature 413, 523-527, 2001
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    Qy
db
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         probable antigenic leucine-rich repeat protein YPO1006 [imported] - Yersinia
C;Species: Yersinia pestis
C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 02-Nov-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               밁
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A;Accession: T01438
A;Status: preliminary; translated from GB/EMBL/DDBJ
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C;Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 05-Nov-1999
C;Accession: T01438
R;Smith, A.; Harmon, G.; Elliott, G.; Twyman, B.
                                                                                                                                                                                                                                                                                                                  A; Molecule type: DNA
A; Residues: 1-291 <K
                                                                                                                                                                                                                                                                                                                                                                                                A;Title: Genome sequence of Yersinia pestis, the causative agent of plague A;Reference number: AB0001; MUID:21470413; PMID:11586360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Note: intron positions not resolved (incomplete sequence)
A;Note: WUGSC:H_GS034D21.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: DNA
A; Residues: 1-843 <SMI>
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                                                                                                                                                                                                                                                                                            A; Cross-references:
                                                                                                                                                                                                                                                                                                                                                         A; Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Cross-references: EMBL:AC003077; NID:g2588634; PIDN:AAB83946.1;
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                                         109 VTSCTFQPLPE----C--LRFVQTNISHL------LKDTCTQLLALKPCIGKACQN 152
      75
                                                                                                                                                                                           Local
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                                                                                                                                                                                                                                                     XP01006
LSSLDLTSLPDTLPPCNELNIICNNLTELPTTLPDNLQTLKASYNQLRTLPNTLPASLLS
                                                                                                              DYPVTVAVNLQDEKHCKALWSLFLAQRWIEQLKTVAG---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GVPD-----NIKSFYKV-----NHIWKFRYDRPFHKGTK-DKENEFKSLWVERTSLYL 529
                                                                                  DRPAATALTPAD---YHAIW-----EKWENDPRTVAGEQRGQAVARMKECLEN-NAERLN 74
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            {\tt PQDMRPLHKKLVDQFFVMKSSLG--IQEFSACMQASPVHFPNGSPRVCRNSAPASVSPDG}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VQSLPGISRWFEVEKREVVEMSPLENAIEVLENKNQQLKTLISQCQTRQMQNINPLTMCL 589
                                                                                                                                                                                                                                                                                                                1-291 <KUR>
                                                                                                                                                                                        Similarity
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                                                                                                                                                                                                                                                                                            GB:AL590842; PIDN:CAC89849.1;
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                                                                                                                                                                                        7.1%; 23.8%;
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                                                                                                                                                                                        Score 87; DB Pred. No. 3.2;
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Pred. No.
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November 1997
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C71617
                                                                                                                                                                                                                            A;Status: preliminary; translated A;Molecule type: DNA A;Residues: 1-181 <WIL>
                                                                                                                                                                                                                                                                                                                                                                          hypothetical protein D1086.1 - Caenorhabditis elegans C; Species: Caenorhabditis elegans C; Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #t
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C;Date: 13-Nov-1998 #sequence_revision 13-Nov-1998 #text_change 21-Jul-2000
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                                                                                                            A; Map position: 5
A; Introns: 112/3;
                                                                                                                                                     A; Gene: CESP: D1086.1
                                                                                                                                                                                         A;Cross-references: EMBL:Z81491; PIDN:CAB04019.1; GSPDB:GN00023; CESP:D1086.1 A;Experimental source: clone D1086
                                                                                                                                                                                                                                                                                   A; Reference number: A; Accession: T20323
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A;Experimental source: clone 3D7
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            54 --LKDYPVTVA-VNLQDEKHCKALWSLFLAQRWIEQLKTVAGSKMQTLLEDVNTEIHFVT
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                                     . Similarity 39; Conserv
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                                     Conservative
                                                                                                                132/3;
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                                                       7.0%;
23.5%;
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                                 b; Score 85; DB
b; Pred. No. 2.8;
24; Mismatches
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Pred. No. 15;
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                                     59;
                                                                      Length 181
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-YPVTVAVNLQD
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                                     44;
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 67
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13 SLLLLLLLSPCLRGTPDCYFSHSPISSNFKVKFRELTDHLLKD----

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presynaptic activity regulator aex-3 - Caenc C; Species: Caenorhabditis elegans C; Date: 03-Dec-1999 #sequence_revision 03-De C; Accession: T37188 R; Leimbac, D.; Minx, M. submitted to the EMBL Data Library, February A; Description: The sequence of C. elegans cc A; Reference number: Z20523 A; Accession: T37188 A. Cteating the company of the company 
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peptidase,
C; Species:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          밁
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C; Superfamily:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: GB:AE004281; GB:AE003852; NID:g9656616; PIDN:AAF95218.1; GSPDB:GN00
A;Experimental source: serogroup O1; strain N16961; biotype El Tor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Title: DNA Sequence of both chromosomes of the cholera A;Reference number: A82035; MUID:20406833; PMID:10952301 A;Accession: E82121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001
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A; Status: translated
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A; Residues: 1-939 <HEI>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           119 -----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       87 LKTVAGSKMQTLLEDVNTE--IHFVTSCTFQ------PLPECLRFVQTNISHLLK 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 40 SNFKVKFRELTDHLLKDY-----PVTVAV-----NLQDEKHCKALWSLFLAQRWIEQ 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8 TILPFLLFLSKAENSPLDCSKDDLQLTVTCRPKLAKLTDEMKKNPLNSGFPSVETLN-KM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SGFSQKLPQLMEVILRKFAQRDFQPKRFATIKQQMTRNWRNAAHDKPISQLFNAMTGLLQ 646
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EKHCKALWSLFLAQRWIEQLKTVAGSKMQTLLEDVNTEIHFVTSC---TFQPLP-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ----PSHP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SLANHLMSATFFHEIRTKQQLGYMVGTGNMPL----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DALRVQGQTYEESLRPLVMLGKS-GTFQR--EVQCQQDDSAIVVYYQSHEVSPRS-IALY 757
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DTC-----TQLLALKPCI--GKACQNFSRCLEVQCQPDSSTL------LPPRSPIAL- 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       insulinase family VC2072 [imported] - Vibrio cholerae (strain N16961
Vibrio cholerae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61;
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GB/EMBL/DDBJ
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H.; Dragoi, I.; Sellers,
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A; Molecule type: mRNA
A; Residues: 1-5, 'R', 7-245, 'A', 247-552 < DEL>
R; Ben-Avram, C.M.; Shively, J.E.; Shadduck, R.K.; Waheed, Proc. Natl. Acad. Sci. U.S.A. 82, 4486-4489, 1985
A; Reference number: A23166; MUID:85242709; PMID:3925458
                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: GB:M81316; GB:M61708; NID:g192802; PIDN:AAA19866.1; R;DeLamarter, J.F.; Hession, C.; Semon, D.; Gough, N.M.; Rothenbuhler, F Nucleic Acids Res. 15, 2389-2390, 1987
A;Title: Nucleotide sequence of a cDNA encoding murine CSF-1 (macrophage A;Reference number: A26575; MUID:87174763; PMID:3494232
A;Accession: A26575
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gene 102, 165-170, 1991
A;Title: Cloning and characterization of the murine promoter A:Reference number: JNO294; MUID:91340149; PMID:1874443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      macrophage colony-stimulating factor precursor - mouse N;Alternate names: colony-stimulating factor 1; M-CSF C;Species: Mus musculus (house mouse) C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
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A;Experimental source: strain Bristol N2; clone C02H7
                                                                                A;Molecule type: protein
A;Residues: 33-39, (CC, 42-57 <BEN>
R;Residues: 33-39, (CC, 42-57 <BEN>
R;Residues: 13-39, (CC, 42-57 <BEN>
A;Residues: 13-71. B; Eng, R; Shadduck, R.K.; Waheed, A.; Ben-Avram, C.M.; Shively, Proc. Natl. Acad. Sci. U.S.A. 84, 1157-1161, 1987
A;Title: Cloning and tissue-specific expression of mouse macrophage colony-stimulatin A;Reference number: A25883; MUID:87147232; PMID:3493488
A;Accession: A25883
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: GB:M21952; GB:J03862; NID:g192804; PIDN:AAA37481.1; R;Harrington, M.A.; Edenberg, H.J.; Saxman, S.; Pedigo, L.M.; Daub, R.; Gene 102, 165-170, 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Title: cDNA cloning and e: A; Reference number: A31401;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Accession: A31401; JN0294; A26575; A23166; A25883 R;Ladner, M.B.; Martin, G.A.; Noble, J.A.; Wittman, V.P.; Proc. Natl. Acad. Sci. U.S.A. 85, 6706-6710, 1988
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A; Residues: 1-13 <HAR>
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A; Accession: JN0294
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A; Residues: 1-552 < LAD>
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A;Cross-references: GB:M15692; NID:g192800; PIDN:AAA37480.1; PID:g192801
                            A; Molecule type: mRNA
A; Residues: 1-2,4-5,'
                                                                                                                                                                                                                                                                     A; Accession: A23166
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LLPAYMPSAE--QLLLAPTPFLIGVPSSFFHHR------KIRELPSDVILVDLD-TNC 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PCIGKACQNFSRCLEVQCQ-PDSSTLLPPRSPIALEATELPEPRPR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DSVDVACRVAMVQFFNSANVFGNFSEHTRTLRLYPRPVVSLQTDSFLRSRPQCTQLIT-D 475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ----IHFVTSC---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LQVPDD-----LYIPDLPEPDATHLKERLKN-AINKMTTMTVDNETSVTDADFGIDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                            'RPR',9-100 <RAJ>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6.9%;
23.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      183/2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           expression of murine macrophage colony-stimulating 1; MUID:88320507; PMID:2457916
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   232/3; 283/3; 386/3; 427/3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 84;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      --TFQPLPECLRFVQTNISHLLKDTCTQLLALK 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 2;
36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            73;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 1409;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                   A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Warren,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   527/3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (macrophage-CSF)
                                                                                                                                                                                                                                                                                                                                                     Rajavashisth,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PID:g192803
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PID:g309199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   699/3;
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4

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Colony-stimulating factor - rat
C.Species: Rattus norvegicus (Norway rat)
C.Species: Rattus norvegicus (Norway rat)
C.Depcies: Rattus norvegicus (Norway rat)
C.Accession: S35703
C.Accession: S35703
C.Accession: S35703
C.Borycki, A.G.: Lenormand, J.L.; Guillier, M.; Leibovitch, S.A.
Biochim. Biophys. Acta 1174, 143-152, 1993
B.Fitle: Isolation and characterization of a cDNA clone encoding for rat CSI
A.Reference number: S35703; MUID:93363632; PMID:8357831
A.Reference number: S35703; MUID:93363632; PMID:8357831
A.Recession: S35703
A.Status: preliminary
A.Molecule type: mRNA
A.Residues: 1-552 cBOR>
A.Residues: 1-552 cBOR>
A.Residues: 1-552 cBOR>
A.Residues: 1-552 cBOR>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Qγ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: EMBL:M84361; NID:g203640; PIDN:AAA03032.1; PID:g203641C;Superfamily: macrophage colony-stimulating factor
                                                                                                                                                                                                                                                                                                      рЬ
                                                                                                                                                                                                                                                                                                                                                     Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Qy
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Search completed: November 24, 2002, 10:12:15 Job time : 17.3755 secs
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 189 CNCLYPKATPSSDPASASPHQPPAP----SMAPLA-----GLAWDDSQR 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     129
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Local Similarity 23.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     71
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                                                                                                                                                                                                                                                                                                         76 DDPVCYLKKAFFLVQDIIDETMRFKDNTPNANATERLQELSNNLN-----SCFTKDYE 128
                                                                                                                                                                                                                                                                                                                                                                                                            18
                                                                                                                                                                                                                                                                                                                                                                                                                                                      12 SSLLLLLLLSPCLRGTPDCYFSHSPISSNFKVKFRELTDHLLKDYPVTVAVNLQDEKH- 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SRLLLYCLLMSRSIAKEVSEHCSHMIGNGHLKV-LQQLIDSQM-ETSCQIAFEFVDQEQL 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SSTLLPPRSPIALEATELPEPRPRQLLLLLLLLPLTLVLLAAAWGLRWQRARR 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DDPVCYLKKAFFLVQDIIDETMRFKDNTPNANATERLQELSNNLN-----SCFTKDYE 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ----CKALWSLFLAQRWIEQL------KTVAGSKMQTLLEDVNTEIHFVTSCTFQPLP 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EQNKACVRTFHETPLQLLEKIKNFFNETKNLLEKDWNIFTKNCNNSFAKCSSRDVVTKPD 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 E----CLR-FVQT-----NISHLLKDTCTQLLALKPCIGKACQN-FSRC--LEVQCQPD 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SSLLLLLLLSPCLRGTPDCYFSHSPISSNFKVKFRELTDHLLKDYPVTVAVNLQDEKH- 70
                                                                                                   CNCLYPKATPSSDPASASPHQPPAP----SMAPLA-----GLAWDDSQR 228
                                                                                                                                                     SSTLLPPRSPIALEATELPEPRPRQLLLLLLLLLLPLTLVLLAAAWGLRWQRARR 217
                                                                                                                                                                                                                                                                                                                                                                                                       SRLLLVCLLMSRSIAKEVSEHCSHMIGNGHLKV-LQQLIDSQM-ETSCQIAFEFVDQEQL 75
                                                                                                                                                                                                       EQNKACVRTFHETPLQLLEKIKNFFNETKNLLEKDWNIFTKNCNNSFAKCSSRDVVTKPD 188
                                                                                                                                                                                                                                                         E----CLR-FVQT-----NISHLLKDTCTQLLALKPCIGKACQN-FSRC--LEVQCQPD 164
                                                                                                                                                                                                                                                                                                                                                          ----CKALWSLFLAQRWIEQL------KTVAGSKMQTLLEDVNTEIHFVTSCTFQPLP 118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6.8%; Score 83.5; DB 1; Length 552; ilarity 23.2%; Pred. No. 14; Conservative 36; Mismatches 94; Indels 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        36;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           94;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 552;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels 49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        49; Gaps
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Result
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Maximum
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Perfect score:
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Maximum Match 100%
Listing first 45 s
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          on:
 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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DB
                                                                                                                                                                                                                                                                                                                                                                                                                  1212.
768.
89.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score
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87
84.5
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length: 2000000000
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1223
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BLOSUM62
Gapop 10.0 , Gapext 0.5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Match
SwissProt_40:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MTVLAPAWSPNSSLLLLLLL....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Copyright
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length
 GenCore version 5.1.3 (c) 1993 - 2002 Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    using
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DВ
                                                                                                                     LEUK, RAT
ALEUK, OUSE
INT. OVIMO
YA4G_SCHPO
YA4G_SCHPO
YM72_MYCTU
RCQ4_HUMAN
POLG_PEMVC
CM35_HUMAN
POLG_PEMVC
CM35_HUMAN
SYES_YEGT
YRG1_YEAST
HB2D_CANFA
GBR2_RAT
YB95_METTH
VS09_ROTS1
ASA1_ENTFA
ASA1_ENTFA
ASA1_ENTFA
                                                                                                                                                                                                                                                                                                                                   AD15_RAT
ATS3_HUMAN
AEX3_CAEEL
CSF1_MOUSE
ZAN_PIG
           DMD_CHICK
PRII_DROME
EPA2_MOUSE
CYB_CAMDR
TRBM_MOUSE
LRP1_CHICK
ENOA_SCEUN
AVR2_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                     FL3L_MOUSE
FL3L_HUMAN
GBR2_HUMAN
AD15_MOUSE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Search time 8.42704 Seconds (without alignments) 1136.939 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .....WQRARRRGELHPGVPLPSHP 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             112892
P28173
Q09173
Q094761
Q094761
Q094700
Q08708
P42837
P42837
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ine; Glycoprotein; Transmembrane; Alternative splicing; Signal.

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SL cytokine precursor (
ligand) (Flt3L).
                                                                                                                                             use by non-profit institutions as lo modified and this statement is not remo entitles requires a license agreement or send an email to license@isb_sib.ch)
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Nat. Struct. Biol. 7:486.491(2000).

-i-FUNCTION: STIMULIATES THE PROLIFERATIO
CELLS. SYNERGIZES WELL WITH A NUMBER
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Hannum C., Culpepper J., Campbell D., McClanahan T., Zurawski S.
Bazan J.F., Kastelein R., Hudak S., Wagner J., Mattson J., Luh J
Duda G., Martina N., Peterson D., Menon S., Shanafelt A.,
Muench M., Kelner G., Namikawa R., Rennick D., Roncarolo M.G.,
Zlotnik A., Rosnet O., Dubreuil P., Birnbaum D., Lee F.;
"Ligand for FLT3/FLK2 receptor tyrosine kinase regulates growth
haematopoietic stem cells and is encoded by variant RNAs.";
Nature 368:643-648(1994).
                                                                                                                                                                                                                                           the European Bioinformatics Institute.
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ALTERNATIVE PRODUCTS: 2 isoforms; a 1/membrane-bound and 2/soluble; are produced by alternative splicing.
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GBR2_HUMAN
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    REAL REPORTS OF THE PROPERTY O
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Best Local
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DISULFID
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CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GBR2_HUMAN STANDARD; PRT; 941
075899; 075974; 075975; Q9UNS9; Q9UNR1; 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF02947;
                                                                                                                                                                                                                                                                                                                                                                                                                Gamma-aminobutyric acid type B receptor, subunit 2 receptor 2) (GABA-B-R2) (Gb2) (GABABR2) (G protein-51) (GPR 51) (HG20).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VARSPLIC
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MEDLINE=20193514; PubMed=10727622;
Clark J.A., Mezey E., Lam A.S., Bonner T.I.;
"Distribution of the GABA(B) receptor subunit gb2
                                                                                                                                                              White J.H., Wise A., Main M.J., Gree Barnes A.A., Emson P., Foord S.M., 1 "Heterodimerization is required for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3D-structure.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro;
                                                                                                                          GABA(B) receptor.";
Nature 396:679-682(1998).
                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. TISSUE=Cerebellum;
                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CARBOHYD
                                                              TISSUE=Brain
                                                                                 PARTIAL SEQUENCE FROM N.A.
                                                                                                                                                                                                                          MEDLINE-99087321; PubMed-9872316;
                                                                                                                                                                                                                                                                                                              NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APTAPQPP---LLLLLLPVGLLLLAAAWCLHWQRTRRRTPRPGEQVPPVPSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ELPEPRPRQLLLLLLLLPLTLVLLAAAWGLRWQRARRR----GELHPGVPLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LREVQTNISRLLQETSEQLVALKPWITR--QNFSRCLELQCQPDSSTLPPPWSPRPLEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LRFVQTNISHLLKDTCTQLLALKPCIGKACQNFSRCLEVQCQPDSSTLLPPRSPIALEAT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MTVLAPAWSP-TTYLLLLLLLSSGLSGTQDCSFQHSPISSDFAVKIRELSDYLLQDYPVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   600007
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HGNC:3766; FLT3LG
                                                                                                                                                                                                                                                                                                                                                                                               OR GPR51
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                                                                                                                                                                                                                                                                                                                                 Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   235 AA;
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                                                                                                                                                                                                                                                                                                                                                                          (Human)
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                                                                                                                                                                                                                                                                                                                                                    Chordata;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17; Mismatches
                                                                                   (ISOFORMS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 768.5; DB 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MISSING (IN ISOFORM 2).
G -> A (IN REF 1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-LINKED (GLCNAC. ..) (POTENTIAL).
N-LINKED (GLCNAC. ..) (POTENTIAL).
DSSTLPPWSRRPLEATA -> VETVFHRVSQDGLDLLTS
(IN ISOFORM 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        POTENTIAL.
CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      POTENTIAL.
SL CYTOKINE
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                                                                                                                                                                                                                                                                                                                                 Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     73B95BF693B4CECF CRC64;
                                                                                                                                                                Green A., Fraser N.J., M., Marshall F.H.; for the formation of a
                                                                                   2A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11 AA.
Q9P1R2;
                                                                                   2в
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                   ubunit 2 precursor (GABA-B protein-coupled receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (POTENTIAL).
                                                                                   AND
                                                                                 2C).
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    rat CNS.
                                                                                                                                                                                                           Disney G.H.
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Martin S.C., Russek S.J., Farb D.H.;
"Molecular identification of the human GABABR2:
expression and coupling to adenylyl cyclase in GABABR1.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Cloning and characterization of a novel human GABA-B recewith high affinity for GABA and low affinity for baclofen submitted (NOV-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ng G.Y.K., Clark J., Coulombe N., Ethier N., Hebert T.E., Sulli Kargman S., Chateauneuf A., Tsukamoto N., McDonald T., Whiting Mezey E., Johnson M.P., Liu Q., Kolakowski L.F. Jr., Evans J.F. Bonner T.I., O'Neill G.P.; Tolakowski L.F. Jr., Evans J.F. and T. G. G. Bababareceptor subunit, gb2, required for functional GABAbareceptor subunit, gb2, required for functional GABAbareceptor activity."; J. Biol. Chem. 274:7607-7610(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Cloning of a novel G-protein-coupled receptor GPR 51 resembling receptors expressed predominantly in nervous tissues and mapped proximal to the hereditary sensory neuropathy type 1 locus on
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            O'Neill G.P., Liu Q.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ng G.Y.K., McDon
Chateauneuf A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (JAN-1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE=Hippocampus;
Borowsky B., Laz T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                           J. Pharmacol. Exp. Ther. 293:460-467(2000).

-i- FUNCTION: RECEPTOR FOR GABA. THE ACTIVITY OF THIS RECEPTOR IS MEDIATED BY G-PROTEINS THAT INHIBITS ADERLYLYL CYCLASE ACTIVITY, STIMULATES PHOSPHOLIPASE A2, ACTIVATES POTASSIUM CHANNELS, INACTIVATES VOLTAGE-DEPENDENT CALCIUM-CHANNELS AND MODULATES INACTIVATES VOLTAGE-DEPENDENT CALCIUM-CHANNELS AND MODULATES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=99189236;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE=Fetal brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Brain Res. 860:41-52(2000)
                                                +
                                                                                                                                                                                                                                                                                                                                    "Coexpression of full-length gamma-aminobutyric Acid(B) (GABA(B)) receptors with truncated receptors and metabotropic glutamate receptor 4 supports the GABA(B) heterodimer as the functional
                                                                                                                                                                                                                                                                                                                                                                                    Sullivan R., Chateauneuf A., Coulombe N
Johnson M.P., Hebert T.E., Ethier N., E
Abramovitz M., O'Neill G.P., Ng G.Y.K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R1A-R2 INTERACTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=99263199; PubMed=10328880;
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                                                                                                                                                                                                                                                                                                                  receptor."
                                                                                                                                                                                                                                                                                                                                  receptor 4 supports the
                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=20237752; PubMed=10773016;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        R1A-R2 INTERACTION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=99175124;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mol. Cell.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5
                                                                                                                                             INOSITOL PHOSPHOLIPIDS HYDROLYSIS. PLAYS A CRITICAL ROLE IN THE FINE-TUNING OF INHIBITORY SYMAPTIC TRANSMISSION. PRE-SYMAPTIC GABA-B-R INHIBIT NEUROTRANSMITER RELEASE BY DOWN-REGULATING HIGH-VOLTAGE ACTIVATED CALCIUM CHANNELS, WHEREAS POSTSYMAPTIC GABA-B-R DECREASE NEURONAL EXCITABILITY BY ACTIVATING A PROMINENT
                               ANTINOCICEPTION.
SUBUNIT: HETEROL
IS EFFECTIVE ON
                                                                              INMARDLY RECTIFYING POYASSIUM (KIR) CONDUCTANCE THAT UNDERLIES LATE INHIBITORY POSTSYNAPTIC POTENTIALS. NOT ONLY IMPLICATED IN SYNAPTIC IN HIPPOCAMPAL LONG-TERM POTENTIATION, SLOW WAVE SLEEP, MUSCLE RELAXATION AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Parker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            56:288-295(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9.=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Neurosci. 13:180-191(1999).
                               HETERODIMER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6; PubMed=10087195; nald T., Bonnert T., Rigby M., Heavens R., Coulombe N., Kargman S., Caskey T., Evans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PubMed=10075644;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (ISOFORM 2A)
MCCrea K., W
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to the
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EMBL/GenBank/DDBJ databases
                               GABA-B-R1 AND GABA-B-R2. AND HOMODIMERIC ASSEMBLY
                                                                                                                                                                                                                                                                                                                                                                                                    Coulombe N., Kolakowski L.F.
thier N., Belley M., Metters
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Watson J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Baker E., Sutherland
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the absence of
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K.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sullivan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          J.F.,
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SUBCELLULAR LOCATION:

INTEGRAL MEMBRANE

PROTEIN.

MOREOVER

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THE THE TREET TH
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VARSPLIC
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TRANSMEM
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InterPro; IPR001337; GPCR_Mgr.
Pfam; PF00003; 7tm_3; 1.
Pfam; PF01094; ANF_receptor; 1.
PROSITE; PS00979; G_PROTEIN_RECEP_F3_1; FALSE_NEG.
PROSITE; PS00980; G_PROTEIN_RECEP_F3_2; FALSE_NEG.
PROSITE; PS00981; G_PROTEIN_RECEP_F3_3; FALSE_NEG.
PROSITE; PS00981; G_PROTEIN_RECEP_F3_4; 1.
G_PROTEIN_RECEP_F3_4; 1.
G_PROTEIN_CECEP_F3_4; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL;
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                                                                                                                                                                                                                                                               CARBOHYD
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SIGNAL
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PRODUCED BY ALTERNATIVE SPLICING.

TISSUE SPECIFICITY: HIGHLY EXPRESSED IN BRAIN, ESPECIALLY IN

CEREBRAL CORTEX, THALAMUS, HIPPOCAMPUS, FRONTAL, OCCIPITAL AND

TEMPORAL LOBE, OCCIPITAL POLE AND CEREBELLUM, FOLLOWED BY CORPUS

CALLOSUM, CAUDATE NUCLEUS, SPINAL CORD, AMYGDALA AND MEDULLA.

WEAKLY EXPRESSED IN HEART, TESTIS AND SKELETAL MUSCLE.

DOWAIN: ALPHA-HELICAL PARTS OF THE C-TERMINAL INTRACELLULAR REGION

MEDIATE HETERODIMERIC INTERACTION WITH GABA-B RECEPTOR 1.

SIMILARITY: BELONGS TO FAMILY 3 OF G-PROTEIN COUPLED RECEPTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             L; AJ012188; CAA09942.1;
L; AF056085; AAC63228.1;
L; AF095723; AAC63383.1;
L; AF095724; AAC63384.1;
L; AF095784; AAD30389.1;
L; AF074483; AAD03336.1;
L; AF069755; AAC99345.1;
L; AF069755; AAC99345.1;
L; AF099033; AAD45867.1;
L; AF099033; AAD45867.1;
L; AF099033; CAD45867.1;
L; AF099047.1;
L; AF099047.1;
L; AF099047.1;
L; AF099047.1;
L; AF099047.1;
L; AF099047.1;
L; AF0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PLASMA MEMBRANE.
ALTERNATIVE PRODUCTS:
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                                                                                                                                                  0259; G_PROTEIN_RECEP_F3_4; 1.
upled receptor; Transmembrane; Glycoprotein; Signal;
membrane; Coiled coil; Alternative splicing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OF GABA-B-R1 AND GABA-B-R2 APPEARS TO BE FOR MATURATION AND TRANSPORT OF GABA-B-R1
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543
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675
691
720
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VI (POTENTIAL).

EXTRACELLULAR (POTENTIAL).

VII (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

COTLED COIL (POTENTIAL).

COILED COIL (POTENTIAL).

N-LINKED (GLCNAC. . ) (POTINICINEL)

N-LINKED (GLCNAC. . ) (POTINICINEL)

N-LINKED (GLCNAC. . ) (POTINICINEL)

N-LINKED (GLCNAC. . ) (POTINICINEL)
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Y -> F.
/FTId=VAR_010148
T -> A.
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III POTENTIAL.
CYTOPLASMIC (POTENTIAL).
IV (POTENTIAL).
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contstation -
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QУ
                                                                                                RA HOWARD L., Nelson K.K., Maciewicz R.A., Blobel C.P.;

RT "Interaction of the metalloprotease disintegrins MDC9 and MDC15 with RT two SH3 domain-containing proteins, endophilin I and SH3PX1.";

RT two SH3 domain-containing proteins, endophilin I and SH3PX1.";

RT two SH3 domain-containing proteins, endophilin I and SH3PX1.";

RT two SH3 domain-containing proteins, endophilin I and SH3PX1.";

RT two SH3 domain-containing proteins, endophilin I and SH3PX1.";

RT two SH3 domain-containing proteins, endophilin I and SH2PX1.";

RT two SH3 domain-containing proteins of the MATURATION.

CC -!- FUNCTION: MAY HE INVOLVED IN CELL-SURFACE PROPELLIA I AND SUBJUNIT: INTERACTS WITH INTEGRIN ALPHAV-BETA3, ENDOPHILIN I AND SORTING NEXIN 9 PREFERENTIALLY

CC -!- SUBJUNIT: INTERACTS WITH INTEGRIN ALPHAV-BETA3, ENDOPHILIN I AND SORTING NEXIN 9 PREFERENTIALLY

CC -!- SUBJUNIT: INTERACTS WITH INTEGRIN OCCURS IN A SECRETORY PATHWAY

CC SUBGESTING THAT THE INTERACTION OCCURS IN A SECRETORY PATHWAY

CC COMPARTMENT PRIOR TO THE MEDIAL GOLGI.

CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN. THE MAJORITY OF THE PROTEIN IS LOCALIZED IN A PERLNUCLEAR COMPARTMENT WHICH MAY

CC CORRESPOND TO THE TRANS-GOLGI NETWORK OR THE LATE ENDOSOME. THE CC PROTEIN IS THE MAJORITY OF THE PROTEIN IN THE CELL SURFACE,

CC WHEREAS THE MAJORITY OF THE PROTEIN IN THE CELL SURFACE,

CC HIESUE SPECIFICITY: HIGHLY EXPRESSED IN HEART, BRAIN, LUNG, AND COMMISSION OF THE PROTESSED AT LOWER LEVELS IN SPLEEN, LIVER, TESTIS AND COMMISSION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 4
AD15_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ър
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Best Local
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O88839; Q9QYL2;
16-OCT-2001 (Re:
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CONFLICT
CONFLICT
SEQUENCE
                                   -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE-Myeloid, and Myeloma;
Shimizu E., Higuchi Y., Matsuura K., Hijiya N., Yamamoto
"Structure of the mouse ADAM 15 (AD56) gene.";
Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=98421554; PubMed=9748307;
Lum L., Reid M.S., Blobel C.P.;
"Intracellular maturation of the mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16-0C7-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
ADAM 15 precursor (EC 3.4.24.-) (A disintegrin and metalloproteinase domain 15) (Metalloproteinase-like, disintegrin-like, and cysteine-rich protein 15) (MDC-15) (Metalloprotease RGD disintegrin protein)
                                                                                                                                                                                                                                                                                                                                                                                                                                                     INTERACTIONS WITH ENDOPHILIN I AND SORTING MEDLINE=20002705; PubMed=10531379;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa: Chordata;
Mammalia; Eutheria: Rodentia;
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MDC15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     rich protein 15) (MD (Metargidin) (AD56).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE=Lung;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADAM15 OR MDC15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16-OCT-2001 (Rel.
15-JUN-2002 (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 183
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Biol. Chem. 273:26236-26247(1998)
                                SORTING NEXIN 9.
DOMAIN: DESINTEGRIN
                                                                     MUSCLE.
DOMAIN: THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PEPRPROLLLLLLLPLTLVLLAAAWGLRWQRARRRGELHPGVPLPSHP 231
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12
424
941 AA;
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                                                                   CYTOPLASMIC DOMAIN INTERACTS WITH
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424
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49.0%;
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                                 DOMAIN BINDS
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S -> R (IN REF. 5).
P -> R (IN REF. 5).
G -> E (IN REF. 3).
MW; 09F1773DB0673C5D C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                 TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   metalloprotease
                                INTEGRIN ALPHAV-BETA3 (BY
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PROSITE; PS00022; EGF_1; FALSE_NEG.
PROSITE; PS01186; EGF_2; 1.
PROSITE; PS00427; DISINTEGRIN_1; FALSE_NEG.
PROSITE; PS50214; DISINTEGRIN_2; 1.
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InterPro; IPR001590; Reprolysin.
InterPro; IPR000130; Zn_MTpeptdse.
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InterPro; IPR000561; EGF-like.
InterPro; IPR001818; Matrixin.
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PROSITE; PS00546; CYSTEINE_SWITCH;
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SIMILARITY: BELONGS TO PEPTIDASE FAMILY M12B.
SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN.
SIMILARITY: CONTAINS 1 DISINTEGRIN DOMAIN.
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THE THE TAIL TO THE PERIPHERAL NERVOUS SYSTEM, PREFERENTIALLY

TO SCHWARM THE PERIPHERAL NERVOUS SYSTEM, PREFERENTIALLY

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C. -:- SUBGESTING THE PERIPHERAL NERVOUS SYSTEM, PREFERENTIALLY
                                                                                                                                                                                                                                                                                                                                        16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
ADAM 15 precursor (EC 3.4.24.-) (A disintegrin and metalloproteinase domain 15) (Metalloproteinase-like, disintegrin-like, and cysteine-rich protein 15) (MDC-15) (Metalloprotease RGD disintegrin protein)
(Metargidin) (CRII-7).
ADAM15 OR MDC15.
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Rattus normegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Rattus.
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Bosse F., Petzold G., Greiner-Pett
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PROSITE: PS00427; DISINTEGRIN_1; FALSE_NEG.
PROSITE: PS00242, DISINTEGRIN_2; 1.
PROSITE: PS00122; EGF_1; FALSE_NEG.
PROSITE: PS00022; EGF_2; 1.
PROSITE: PS00146; EGF_2; 1.
PROSITE: PS00146; EGF_2; 1.
PROSITE: PS00146; CYSTEINE_SWITCH; FALSE_NEG.
PROSITE: PS00546; CYSTEINE_SWITCH; FALSE_NEG.
PROSITE: PS00546; CYSTEINE_SWITCH; Signal; Glycoprotein; Zymogen;
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InterPro; IPR000130;
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SIMILARITY:
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INDUCTION: IN RESPONSE TO SCIATIC NERVE INJURY
DOMAIN: THE CYTOPLASMIT FORMATM TOWNSTON TO SERVE INJURY
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PTM: THE PRECURSOR
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DOMAIN: DESINTEGRIN DOMAIN BINDS
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SH3-BINDING (POTE
CYSTEINE SWITCH.
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EGF-LIKE.
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RESULT 6
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                                                                                                           Nagase T., Ishikawa K.-I., Nakajima D., Ohira M., Seki Miyajima N., Tanaka A., Kotani H., Nomura N., Ohara O., "Prediction of the coding sequences of unidentified hur The complete sequences of 100 new cDNA clones from bra: code for large proteins in vitro.";
DNA Res. 4:141-150(1997).
-!- FUNCTION: Cleaves the propeptides of type II collactibrial assembly. Does not act on types I and III coll-copactors. BINDS 1 ZINC ION (By SIMILARITY).
-!- SUBCELLULAR LOCATION: Secreted. Associated with the
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015072; Q9BXZ8;
16-OCT-2001 (Rel. 40, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
ADAMTS-3 precursor (EC 3.4.24.-) (A disintegrin and metalloproteinase with thrombospondin motifs 3) (ADAM-TS 3) (ADAM-TS 3) (Procollagen II
                                                                                                                                                                                                                                        MEDLINE=97349984; PubMed=9205841;
Nagase T., Ishikawa K.-I., Nakajima
                                                                                                                                                                                                                                                                   TISSUE-Brain;
                                                                                                                                                                                                                                                                                  SEQUENCE OF 5-1205
                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=21402912;
Fernandes R.J., H
                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                            dermatosparaxis.
                                                                                                                                                                                                                                                                                                                             Eyre D.R., Apte S.S.;
"Procollagen II amino
dermatosparaxis.";
                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 1-227
                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens (Human)
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SIMILARITY:
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                                       TISSUE SPECIFICITY: Found in cartilage and skin. DOMAIN: THE SPACER DOMAIN AND THE TSP TYPE-1 DOM FOR A TIGHT INTERACTION WITH THE EXTRACELLULAR WE PIM: THE PRECURSOR IS CLEAVED BY A FURIN ENDOPEE
                                                                                 matrix (By similarity).
TISSUE SPECIFICITY: Fou
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                                                                                                                                                                                                                                                                                                                                                               Engle J.M.,
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A FURIN ENDOPROM
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PROSITE; PSD01427; DISINTEGRIN_1; FALSE_NEG.
PROSITE; PSD0427; DISINTEGRIN_1; FALSE_NEG.
Hydrolase; Metalloprotease; Zinc; Signal; Glycoprotein; Zymogen; Hydrolase; Metalloprotease; Zinc; Signal; Glycoprotein; Zymogen;
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METAL
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                           VLCRAGDHCDGEKPESVRACQLPPCNDEPCLGDKSIFCQMEVLARYCSIPGYNKLCCESC
                                                                                    ---MOTLLEDVNTEIHFV----
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49; Conser
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                                                                                                                                                                                                                                                                                                      entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-Bristol N2;
MEDLINE-97282461;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Caenorhabditis elegans.
                                                                                                                                                                           Pfam; PF02141; DENN; 1. Pfam; PF03455; dDENN; 1. Pfam; PF03456; uDENN; 1.
                                                                                                                                                                                                                                                                   EMBL; U93842; AAB52421.1; EMBL; U49945; AAC47926.1;
                                                                                                                                                                                                                                                                                                                                modified and this statement
                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produbetween the Swiss Institute of Bioinformatics the European Bioinformatics Institute. There
                                                                                                                                                                                                                                                                                                                                                                                                                                                              in synaptic transmission.";
EMBO J. 19:4806-4816(2000).
-!- FUNCTION: GUANINE NUCLEOTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Leimbac D., Minx M.;
Submitted (FEB-1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-Bristol N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Iwasaki K., Staunton J., Saifee O.,
"aex-3 encodes a novel regulator of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=6239;
                                                                                                                            SEQUENCE
                                                                                                                                                                Guanine-nucleotide releasing
                                                                                                                                                                                                                                                       WormPep;
                                                                                                                                                                                                                                                                                                                                                                                                            -!- TISSUE SPECIFICITY: EXPRESSED IN A VARIETY OF NEURONS -!- SIMILARITY: CONTAINS 1 DENN DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Iwasaki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=20428446; PubMed=10970871;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INTERACTION WITH CAB-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Neuron 18:613-622(1997).
                                                                                                                                          DOMAIN
                                                                                                                                                    DOMAIN
                                                                                                                                                                                                                              InterPro;
                                                                                                                                                                                                                                         InterPro;
                                                                                                                                                                                                                   InterPro;
                          317
 63
                                                                                       Local
                                                 4
                                                                                                                                                                                                                                                                                                                                                                                                                                      SUBUNIT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                   REGULATE TWO DIFFERENT PATHWAYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         aki K., Toyonaga k., rab3 GDP/GTP exchange factor homolog
                                                 LAPAWSPNSSLLLLLLLLSPCLRGTPDCYFSHSPISSNFKVKFREL-TDHLLKDYPVTVA
VNLQDEKHCKALWSLFL ---
                        LLPAYMPSAE - - QLLLAPTPFLIGVPSSFFHHR - -
                                                                                        Similarity
                                                                                                                                                                                                                                                       C02H7.3;
                                                                                                                                                                                                                  IPR005113; uDENN
                                                                                                                                                                                                                              IPR001194; DENN. IPR005112; dDENN
                                                                                                                            1409
                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                       BINDS TO CAB-1
                                                                                                                                                                                                                                                                  AAB52421.1; -.
AAC47926.1; -.
                                                                                                                            AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PubMed=9136770;
                                                                                                                                                                                                                                                       CE16806.
                                                                                                                                          632
                                                                                                                                                      364
                                                                                                                                                                                                                                                                                                                                               institutions as long as its content
                                                                                       6.9%;
23.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    to the EMBL/GenBank/DDBJ databases
                                                                                                                            157458 MW;
                                                                        31;
                                                                                                                                                                                                                                                                                                                                     is not removed.
                                                                                       Score 84;
Pred. No.
 AQRWIEQLKTVAGSKMQTLLEDVNTE---
                                                                                                                                          SER-RICH
                                                                                                                                                       DENN
                                                                                                                                                                factor.
                                                                           Mismatches
                                                                                                                            2DDE6395AC963313 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                EXCHANGE
                                                                                                                                                                                                                                                                                                                                                                           It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                    FOR NEURAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nonet M., Thomas J.H. presynaptic activity
                                                                                                                                                                                                                                                                                                                                                         There are no restrictions
                                                                                                   DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                FACTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AEX-3 has a dual function
                                                                                                    1;
                                                                                                                                                                                                                                                                                                                                  Usage
                                                                           73;
                          KIRELPSDVILVDLD-TNC
                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACTIVITIES
                                                                                                    Length 1409;
                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                FOR
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                                                                           Gaps
                          365
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RESULT 8

CREP1_MOUSE
ID CSSP1_MA
AC P07141
DT 01-FEB
RT 01-FEB
RT
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SEQUENCE
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P07141;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-87147232; PubMed=3493488;
Rajavashisth T.B., Eng R., Shadduck R.K., Waheed A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30-MAY-2000 (Rel. 33, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
Macrophage colony stimulating factor-1 precursor
CSF1 OR CSFM.
                                                                                            CSF-1 gene.
                                                                                                        Borycki A.G., Lenormund J., Guillier M., Leibovitch S.A.; "Isolation and characterization of a cDNA clone encoding for rat
                                                                                                                                                                                                                                                                                                                               Ben-Avram C.M., Shively J.E., Shadduck R.K., Rajavashisth T.B., Lusis A.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=88320507; PubMed=2457916;
Ladner M.B., Martin G.A., Noble J.A., Wittman V.P., Warren M.K.,
McGrogan M., Stanley E.R.;
"CDNA cloning and expension of murine macrophage colony-stimulating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                Biochim.
                                                                 differentiation.",
                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=85242709; PubMed=3925458;
                                                                                                                                                                                                                                                                                                                                                                                                        SPECIES=Mouse;
                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 33-57.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Cloning and tissue-specific expression stimulating factor mRNA.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Shively J.E., Lusis A.J.;
                                                                                                                                                              MEDLINE=93363632; PubMed=8357831;
                                                                                                                                                                                              SPECIES-Rat;
                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 1-100 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nucleic Acids Res. 15:2389-2390(1987)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Nucleotide sequence of a cDNA encoding (Macrophage-CSF).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mermod
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Delamarter J.F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=87174763;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-APR-1988 (Rel. 07, Created)
01-FEB-1996 (Rel. 33, Last seq
30-MAY-2000 (Rel. 39, Last ann
                                                                                                                                                                                                                                                                                                         Amino-terminal amino
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=10090, 10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus (Mouse), and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    144
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PCIGKACQNFSRCLEVQCQ-PDSSTLLPPRSPIALEATELPEPRPR
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    OF 1-13
                                           Biophys.
                                                                                          Post-transcriptional
                                                                                                                                                                                                                                                             Acad.
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                                                                                                                                                                                    STRAIN-Wistar;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                         Acta 1174:143-152(1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hession
                                                                                                                                                                                                                                                             Sci.
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Hession C., Semon
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sci. U.S.A.
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                                                                                                                                                                                                                                                          U.S.A. 82:4486-4489(1985)
                                                                                                                                                                                                                                                                                                 sequence of murine colony-stimulating
                                                                                                                                                                                    TISSUE=Muscle;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 85:6706-6710(1988).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Craniata;
                                                                                  repression occurs in myogenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -TFQPLPECLRFVQTNISHLLKDTCTQLLALK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              macrophage colony
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (CSF-1) (MCSF).
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EMBL; M21952; AAA37481.1;
EMBL; M21149; AAA37482.1;
EMBL; M15692; AAA37480.1;
EMBL; M84361; AAA03032.1;
EMBL; M81316; AAA19866.1;
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CARBOHYD
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DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PIR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cytokine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              entities requires a license agreement (S or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIGNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Cloning and characterization of the murine promoter stimulating factor-1-encoding gene."; Gene 102:165-170(1991).
                                                                                                                                     119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                the European Bioinformatics Institute.
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                                                                                           129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Harrington M.A., Edenberg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SPECIES=Mouse;
  189 CNCLYPKATPSSDFASASPHQPPAP----SMAPLA----
                                                                                                                                                                               76
                                                                                                                                                                                                                       71
                                                                                                                                                                                                                                                                    18
                                                                                                                                                                                                                                                                                                         12
                                                                                                                                                                                                                                                                                                                                                                          Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FUNCTION: GRANULOCYTE/MACROPHAGE COLONY-STIMULATING FACTORS ARE CYTOKINES THAT ACT IN HEMATOPOLESIS BY CONTROLLING THE PRODUCTION, DIFFERENTIATION, AND FUNCTION OF 2 RELATED WHITE CELL POPULATIONS OF THE BLOOD, THE GRANULOCYTES AND THE MONOCYTES-MACROPHAGES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FUNCTION: THIS CSF INDUCES MACROPHAGES.
SUBUNIT: HOMODIMER, LINKED BY THREE DISULFIDE BONDS
                                          SSTLLPPRSPIALEATELPEPRPRQLLLLLLLLPLTLVLLAAAWGLRWQRARR 217
                                                                                                                                                                        DDPVCYLKKAFFLVQDIIDETMRFKDNTPNANATERLQELSNNLN-----
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                                                                                    EQNKACVRTFHETPLQLLEKIKNFFNETKNLLEKDWNIFTKNCNNSFAKCSSRDVVTKPD
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MGI:1339753; C
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Edenberg H.J., Saxman S.M., Pedigo L.M., Daub R.,
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AG -> PR (IN REF. 3).
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W; 3886D72D70E770AF CRC64;
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Pred. No. 6.2;
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RESULT 9
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J. Biol. |
-!- FUNCT
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1658-1667;
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HSSP;
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                                                                                                                                                                                                                                                                                             the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                    This
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Mammalia; |
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                                                                                                                           Pfam;
                                                                                                                                                                                                                                                                 or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                entities requires a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A sperm membrane protein that binds in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUBUNIT: PROBABLY FORMS COVALENT OLIGOMERS.
SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN, EXCLUSIVELY ON T
SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN, EXCLUSIVELY ON T
APICAL REGION OF THE SPERM HEAD (BY SINILIARITY).
TISSUE SPECIFICITY: IN TESTIS, PRIMARILY IN HAPLOID SPERMATIDS.
NOT IN LUNG, LIVER, HEART, SPLEEN, BRAIN, KIDNEY, EPIDIDYMIS.
DOMAIN: THE MAM DOMAINS PROBABLY MEDIATE SPERM ADHESION TO THE
ZONA PELLUCIDA.
                                                                                                                                                                                                                                                                                                                                                                                                                                               THE MUCIN-LIKE DOMAIN MIGHT INHIBIT INAPPROPRIATE TRAPPING OF SPERMATOZOA OR PROMOTING ADHESION TO THE OVIDUCTAL ISTHMUS. DOMAIN: THE VWPD DOMAINS 2 AND 3 MAY MEDIATE COVALENT OLIGOMERIZATION (BY SIMILARITY TO HUMAN INTESTINAL MUCIN MUC2). FROM THE MAM DOMAINS AND THE MUCIN-LIKE DOMAINS ARE MISSING FROM THE ZONADHESIN THAT BINDS TO THE EGG EXTRACELLULAR MATRIX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   scrofa
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                                                                                                                                                                                                                                                                                                                                                                                                                        CAPACITATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                      PROCESSING
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                              ; PF00094; vwd; 4.
; PF00659; MAM; 2.
; PF01826; TIL; 5.
; PF01345; TILa; 5.
; PF02345; TILa; 5.
; SM00181; EGF; 17; SM00137; WWC; 2.
T; SM00216; VWD; 4.
                                                                                                                                                                                                                                                                                                                                     SWISS-PROT entry is copyright. It is produced through a collaboration sen the Swiss Institute of Bioinformatics and the EMBL outstation.
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NCTION: BINDS IN A SPECIES-SPECIFIC MANNER TO THE ZONA
THE EGG. MAY BE INVOLVED IN GAMETE RECOGNITION AND/OR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FROM N.A., AND SEQUENCE OF 823-830; 859-872; 883-890; 960-967; 1235-1244; 1349-1354; 1518-1532; 1624-1656; 7; 1777-1795 AND 1914-1921.
                                                                                                                                         IPR003328;
IPR001007;
IPR001846;
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IPR000998;
IPR002919;
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EGF_2;
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TILa_Cysrich.
VWF_C.
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בייתייבי, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae، אייריים NCBI_TaxID=10116;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUB-Thymocytes;
MEDLINE-8816646; PubMed-2965006;
Killeen N., Barclay A.N., Willis A.C., Williams A.F.;
"The sequence of rat leukosialin (W3/13 antigen) reveals a molecule with o-linked glycosylation of one third of its extracellular amino
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PIR; S00842;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a converge the Swiss Institute of Bioinformatics and the EMBL
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SEQUENCE FROM N.A.
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STRUCTURES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GLYCAN CHAINS TO BE ACCESSIBLE FOR BINDING. SUBCELLULAR LOCATION: Type I membrane protein. TISSUE SPECIFICITY: CELL SURFACE OF THYMOCYTES, NEUTROPHILS, PLASMA CELLS AND MYELOMAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EVINCTION: ONE OF THE MAJOR GLYCOPROTEINS OF THYMOCYTES AND T
LYMPHOCYTES. PLAYS A ROLE IN THE PHYSICOCHEMICAL PROPERTIES OF
THE T-CELL SURFACE AND IN LECTIN BINDING. PRESENTS CARBOHYDRATE
LIGANDS TO SELECTINS. HAS AN EXTENDED RODLIKE STRUCTURE THAT COULD
PROTRUDE ABOVE THE GLYCOCALYX OF THE CELL AND ALLOW MULTIPLE
       APASSIPL --
                                     SPNSSLLLLLLLSPCLRGTPDC---YFSHSPISSNFKVKFRELT-----
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                                                                                               Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HAS A HIGH CONTENT OF SIALIC ACID AND O-LINKED CARBOHYDRATE
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-GTPELSSFFFTSAGASGNTPVP--ELTTSQEVSTEASLVLFP 106
                                                                                                                                                    MW;
                                                                            24;
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4; Mismatches
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""" "Genetic variation in mouse apolipoprotein A-IV due to insertion and ref deletic variation in a region of tandem repeats.";

RI J. Biol. Chem. 266:12715-12721(1991).

CC -i- FUNCTION: MAY HAVE A ROLE IN CHYLOMICRONS AND VLDL SECRETION AND CC CATABOLISM. REQUIRED FOR EFFICIENT ACTIVATION OF LIPOPROTEIN CC LIPASE BY APOC-II; POTENT ACTIVATION OF LIPOPROTEIN CC LIPASE BY APOC-II; POTENT ACTIVATION OF LCAT. APOA-IV IS A MAJOR CC COMPONENT OF HDL AND CHYLOMICRONS.

CC -I- SUBCELLULAR LOCATION: EXERGELULAR.

CC -I- SUBCELLULAR LOCATION: EXERGELULAR COLOR THE THIRTEEN 22-AMINO ACID TANDEM REPEATS (EACH 22-MERIS) COCURRING IN THIS SEQUENCE ARE PREDICTED TO BE HIGHLY ALPHA-CC MERS) OCCURRING IN THIS SEQUENCE ARE AMPHIPATHIC. THEY MAY THEREFORE SERVE AS LIPID-BINDING DOMAINS WITH LECITHIN:CHOLESTEROL ACYLTRANSFERASE (LCAT) ACTIVATING ABILITIES.

C -I- POLYMORPHISM: THERE IS A POLYMORPHISM WITHIN A SERIES OF IMPERFECT OF POLYMORPHISM: THERE IS A POLYMORPHISM WITHIN A SERIES OF IMPERFECT OF 12 NUCLEOTIDES HAVE GIVEN RISE TO THREE FORMS CHARACTERIZED BY THREE (139), FOUR (C57BL/6), OR FIVE (M.CASTANEUS) COPIES OF THE SEQUENCE E-Q-(AVI-Q-). INSERTIONS OR DELETIONS OR DELETIONS OF IMPERFECT OF THE SEQUENCE E-Q-(AVI-Q-). INSERTIONS OF THE SEQUENCE E-Q-(AVI-Q-). INSERTIONS OR DELETIONS OF THE SEQUENCE E-Q-(AVI-Q-). INSERTIONS OF THE SEQUENC
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation between the Swiss Institute of Bioinformatics and the EMBL outstation on its
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=C57BL/6J, important strain (STRAIN) (STRAINN) (STRAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-JAN-1988 (Rel. 06, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
Apolipoprotein A-IV precursor (Apo-AIV).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Reue K., Leete
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a high-lipid diet.";
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                                                                                                                                               SIMILARITY: BELONGS TO THE APOA1 / APOA4 / APOE FAMILY.
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P28172;
30-MAY-2000
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                                                                                                               P28172;
30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
30-MAY-2000 (Rel. 39, Last annotation update)
Interferon tau precursor (IFN-tau) (Trophoblast antiluteolytic prot
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CONFLICT
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                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovidae; Caprinae; Ovibos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
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REPEAT
                                                                                                       Ovibos moschatus (Muskox)
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             NCBI_TaxID=37176;
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                                                                                                                                                                                                                                                                                                                                                                                                            PLPECLREVQTNISHLLKDTCTQLLALKPCIGKACQNFSRCLEVQCQPDSSTLLP 170
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                                                                                                                                                                                                                                                                                                                                                                           QL-----QKNLAPLVEDVQSKVKGNTEGLQKSLEDLNRQLEQQVEEFRRTVEP 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                            ELKATIDQNLEDLRRSLAPLTYGYQEKLNHQMEGLA-FQMKKNAEELQTKY----SAKID
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E -> R (IN REF. 1).
S -> A (IN REF. 1).
RQ -> KA (IN REF. 1).
NK -> GG (IN REF. 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 80.5; I
Pred. No. 7.8;
12; Mismatches
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                                                                                      DISULFID CARBOHYD
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-!- TISSUE SPECIFICITY: CONSTITUTELY AND EXCLUSIVELY EXPRESSED IN THE MONONUCLEAR CELLS OF THE EXTRA-EMBRYONIC TROPHECTODERM.
-!- DEVELOPMENTAL STAGE: MAJOR SECRETORY PRODUCT SYNTHESIZED BY THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "IFN-tau: a novel subtype I IFN1. Structural characteristics, non-ubiquitous expression, structure-function relationships, a pregnancy hormonal embryonic signal and cross-species therapeutic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   and
                                                                      SEQUENCE
                                                                                                                                            CHAIN
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use by non-profit institutions as 10
modified and this statement is not remo
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-!- FUNCTION: PARACRINE HC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=99081096; PubMed=9865498;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. MEDLINE=92242937; PubMed=1374107;
                                                                                                                         DISULFID
                                                                                                                                                             SIGNAL
                                                                                                                                                                                                                                                 PRINTS; PR00266;
                                                                                                                                                                                                                                                                                                                                                                                                                                            between
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Leaman D.W., Roberts R.M.;
"Genes for the trophoblast interferons in sheep, and distribution of related genes among mammals."
J. Interferon Res. 12:1-11(1992).
                                                                                                                                                                           Pregnancy;
                                                                                                                                                                                                PROSITE; PS00252;
                                                                                                                                                                                                                                                                  Pfam; PF00143; interferon;
                                                                                                                                                                                                                                                                                 InterPro; IPR000471; Interferon_abd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REVIEW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RECEPTOR EXPRESSION IN THE ENDOMETRIUM. THIS RESULTS IN THE SUPPRESSION OF THE DUISATILE ENDOMETRIAL RELEASE OF THE LUTEOLYTIC SUPPRESSION OF THE FULSATILE ENDOMETRIAL RELEASE OF THE LUTEOLYTIC HORMONE PROSTAGLANDIN EZ-ALPHA, HINDERING THE REGRESSION OF THE CORPUS LUTEUM (LUTEOLYSIS) AND THEREFORE A RETURN TO OVARIAN VYCLICITY. THIS, AND A POSSIBLE DIRECT EFFECT OF IFN-TAU ON PROSTAGLANDIN SYNTHESIS, LEADS IN TURN TO CONTINUED OVARIAN PROGESTERONE SECRETION, WICH STIMULATES THE SECRETION BY THE ENDOMETRIUM OF THE NUTRIENTS REQUIRED FOR THE GROWTH OF THE CONCEPTUS. IN SUMMARY, DISPLAYS PARTICULARLY HIGH ANTIVIRAL AND ANTIPROLIFERATIVE POTENCY CONCURRENTLY WITH PARTICULAR WEAK CYTOTOXICITY, HIGH ANTILUTEDLYTIC ACTIVITY AND IMMUNOMOULLATORY OF THE NUTRIENT THE CONCEPTUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               THEY ENCODE FOR PROTEINS VERY SIMILAR IN SEQUENCE BUT WITH DIFFERENT BIOLOGICAL POTENCY AND PATTERN OF EXPRESSION. SIMILARITY: BELONGS TO THE INTERFERON ALPHA, BETA AND DELTY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CONCEPTUS DURING A VERY SHORT PERIOD IN EARLY PREGNANCY.
MISCELLANEOUS: IRN-TAU GENES ARE INTRONLESS. THEY EVOLUED FROM
IFN-OMEGA GENES IN THE RUMINANTIA SUBORDER AND HAVE CONTINUED TO
DUPLICATE INDEPENDENTLY IN DIFFERENT LINEAGES OF THE RUMINANTIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FUNCTION: PARACRINE HORMONE PRIMARLY RESPONSIBLE FOR MATERNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RECOGNITION OF PREGNANCY. I PROBABLY TYPE I INTERFERON EXPRESSION, PREVENTING THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FAMILY. IFN-ALPHAII SUBFAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                          SWISS-PROT entry is copyright. It is produced through a c
een the Swiss Institute of Bioinformatics and the EMBL
European Bioinformatics Institute. There are no restrict
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                                                                                                                                                                                                                                                                                                                    M73244; AAA31583.1;
                                                                                                                                                                                                              SM00076;
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                                                                                                                                                                           Cytokine;
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                                                                      AA;
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27.4%;
                                                                                                                                                                             Hormone;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Huynh L.P., L'Haridon R.M.,
M.A., Charpigny S.Y.;
                                                                        MW.
                                                                                   e; Antiviral; Sign
BY SIMILARITY
INTERFERON TAU.
BY SIMILARITY
BY SIMILARITY.
BY SIMILARITY.
CONTROL (GLCNAC)
                                 Score 80;
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                                                                                                                                                                                                                                                                                                                                                                      (See http://www.isb-sib.ch/announce/
                                                                                      (GLCNAC
                                   DB 1;
                                                                                                                                                                           Signal;
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                               Length 195;
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                                                                        CRC64;
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                                                                                                                                                                        Glycoprotein
                                                                                    (POTENTIAL)
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l Similarity 34; Conser

Conservative

.48;

Pred.

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9

17;

Mismatches No

33,

Indels

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Gaps

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RESULT 13
YA4G_SCHPO
                                                                                                                                                                                                                                                                                                                  RA Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
RA Sgouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., McLean J.,
RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., McLean J.,
RA Holroyd S., Hornsby T., Howarth S., McDonald S., McLean J.,
RA Holroyd S., Hornsby T., Howarth S., WcLean J.,
RA Holroyd S., Hornsby T., Howarth S., WcDonald S., McLean J.,
RA Holroyd S., Hornsby T., Howarth S., WcLean J.,
RA Rother K., Tylor R.G., Tivey A., Walsh S.V., Warren T., Whithehead S.,
RA Rylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whithehead S.,
RA Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,
RA Weltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
RA Weltjens I., Vanstreels E., Rieger M., Schaefer M., Hilbert H.,
RA Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T M.,
RA Galble C., Fuchs M., Fritzc C., Holzer E., Moore K., Hurst S.M.,
RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
RA Lucas M., Rochet M., Galilardin C., Tallada V.A., Garzon A., Thode G.,
RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
RA Cerrutti L., Lowe T., McCombie W.R., Paulsen I., Potsburg S.L.,
RA Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.;
"The genome sequence of Schizosaccharomyces pombe.";
RT Nature 415:871-880(2002).
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01-NOV-1995 (Rel. 32, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Hypothetical protein C31A2.16 in chromosome
SPAC31A2.16.
                                                                                                                           entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                      between the Swiss Institute of Bioinformatics and the EMBL outstat
the European Bioinformatics Institute. There are no restrictions on
use by non-profit institutions as long as its content is in no
                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration
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                                                                                     EMBL; Z50113; CAA90474.1; -.
                                                                                                                                                                      modified and this statement is not removed.
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Q09733;
                                        InterPro; IPR001331; GDS_CDC
InterPro; IPR000219; RhoGEF.
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Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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RESULT 14
YM72_MYCTU
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Best Local Similarity
                                                                                                                                                                                                                                                                   Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Squares R., Sulston J.E., Taylor K., Whitehead S., Barrell B.G., "Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence.";
                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                             Fleischmann R.D., Alland D., Eisen J.A., Carpenter I., White O., Peterson J., DeBoy R., Dodson R., Gwinn M.I., Haft D., Hickey E., Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula
                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN=CDC 1551 / Oshkosh;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteria; Actinobacteria; Actinobacteria (class); Actinobacteridae; Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium NCBI_TaxID=1773;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Hypothetical protein Rv2272.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE;
                                                                                                    Submitted (APR-2001) to the
                                                                                                                                                   Bishai W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. STRAIN=H37RV;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mycobacterium tuberculosis
                                                                                                                    laboratory strains.
                                                                                                                      "Whole genome comparison of Mycobacterium tuberculosis clinical and laboratory strains.";
                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=98295987;
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                                                                     SUBCELLULAR LOCATION: Integral membrane SIMILARITY: TO E.COLI YIDH.
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RESULT 15
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Best Local :
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                                                                              This
                                                                                                                                                                Genomics 61:268-276(1999).

1. SUBCELLULAR LOCATION: Nuclear (Potential).

1. DISEASE: DEFECTS IN RECQL4 ARE A CAUSE OF ROTHMUND-THOMSON

SYNDROME (RTS). A DISEASE CHARACTERIZED BY DERMAROLOGICAL FEATURES

SUCH AS ATROPHY, PIGMENTATION, AND TELANGIECTASIA AND FREQUENTLY

ACCOMPANIED BY JUVENILE CATARACT, SADDLE NOSE, CONGENITAL BONE
                                                                                                                                                                                                                                                                                                                                                         MEDLINE-99097344; pubMed=9878247; Kitao S., Ohsugi I., Ichikawa K., Goto M., Furuichi Y., Shimamoto A.; "Cloning of two new human helicase genes of the RecQ family: biological significance of multiple species in higher eukaryotes."; Genomics 54:443-452(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TRANSMEM
SEQUENCE
                                                the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      JU-MAY-2000 (Rel. 39, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
ATP-dependent DNA helicase Q4 (RecQ protein-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL;
                                                                                                                                                                                                                                                                                               MEDLINE=20021764; PubMed=10552928;
Kitao S., Lindor N.M., Shiratori M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last seg
15-JUN-2002 (Rel. 41, Last ann
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                                                                                                                                                                                                                                                             products.";
                                              European Bioinformatics Institute.
                                                                                                   DEFECTS, DISTURBANCES OF HAIR GROWTH, AND HYPOGONADISM.
SIMILARITY: BELONGS TO THE HELICASE FAMILY. RECQ SUBFAMILY.
DATABASE: NAME-Atlas Genet. Cytogenet. Oncol. Haematol.;
WWW="http://www.infobiogen.fr/services/chromcancer/Genes/RECQL4ID285.html".
                                                        SWISS-PROT entry is copyright. It is produced through a collaboration sen the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TSGMGLLRWQQADRAMRRH--LPLPRHP
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hetical protein; Transmembrane; Complete proteome.

MEM 33 53 POTENTIAL.

MEM 58 78 POTENTIAL.

MEM 97 117 POTENTIAL.

NCE 122 AA; 12994 MW; 23A53754264887A7 CRC64;
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29; Conservative
non-profit institutions as long and this statement is not removed requires a license agreement (See
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responsible gene, RECQL4: genomic st
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; 23A53754264887A7
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Pred. No. 3.
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http://www.isb-sib.ch/announce/
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Pfam; PF00271; helicase_C; 1.
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MCSRER-RRVQRAFMQGQLRVVVATVAFGMGLDRPDVRAVLHLGLP-PS
                                                                   ALKPCIGKACQNFS-
                                                                                                                                  ALVGAGGLPPAAQLPPVAFACIDEAHCLSQWSHNFRPCYLRVCKVLRERMGVHCFLGLTA 642
                                                                                                                                                                                                                                                                                                                                                                                                                                    268400;
                                          TLLQ--GKRFQNLDSIIIYCNRREDTERIAALLRTCLHAAWVPGSGGRAPKTTAEAYHAG
                                                                                                                                                                                 SPCLTLVVSPLLSLMDDQVSGLPPCLKAACIHSGMTRKQRESVLQKIRAAQVHVLMLTPE
                                                                                                                                                                                                   SPNSSLLL--LLLLLSPCLRGTPDCYFS---HSPIS----SNFKVKFRELTDHLLKDYPV
                      ELPEPRPRQLLLLLLLPLTLVLLAAAWGLRWQRARRRGELHPGVPLPS
                                                                                       TATRRTASDVAQHLAVAEEPDLH------GPAP-----VPTNL-HLSVSMDRDTDQALL
                                                                                                            ----AGSKMQTLLEDVNTEIHFVTSCTFQPLPECLRFVQTNISHLL----KDTCTQLL
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SM00490; HELICC; 1.
SM00343; ZnF_C2HC; 1.
MS; TIGR00614; recq; 1.
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Search completed: November 24, 2002, 10:10:43 Job time: 12.427 secs

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Q9H665
Q9BGY6
Q9ASP5
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2 Q83443
2 Q83448
Q9H563
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Q8VCH4
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Q9bgy6 macaca fasc
Q9asp5 arabidopsis
Q83443 murine rota
Q83448 murine rota
Q9h563 homo sapien
Q94824 homo sapien
Q14584 homo sapien
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Q8vch4
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Q9gkd9 bos taurus
Q42484 arabidopsis
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Q9h9u7 homo sapien	Q91s68 arabidopsis		Q9dby4 mus musculu	Q9sn38 arabidopsis	Q9t7t9 tapirus ind	Q9zy32 orycteropus		2	Q9vnp5 drosophila	Q8t0n4 drosophila	Q9w2d7 drosophila	Q9umt2 homo sapien	Q9b6d1 yarrowia li	Q9n4u7 caenorhabdi			Q9mbf8 chlamydomon	006521 enterococcu	_			Q9i802 drosophila	Q.	Q8zh99 yersinia pe	Q9fke2 arabidopsis	Q9cyb2 mus musculu		Q8sxa6 drosophila

## ALIGNMENTS

RESULT 1 Q61104

Q61104; Q61104; 01-NOV-1996 ( 01-NOV-1996 ( 01-JUN-2002 ( Flt3 ligand,

6 (TrEMBLrel. (6 (TrEMBLrel. (2 (TrEMBLrel. )2 (TrEMBLrel. )3, T169 form.

01, 01, 21,

Created)
Last sequence update)
Last annotation update)

PRELIMINARY;

PRT;

172 AA

Mus musculus (Mouse).

Mus

FLT3L.

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Best Local S
Matches 165
                                                                                                                                                    forms and processing.";
Submitted (DEC-1995) to the EMBL/GenBank/DDBJ databases.
EMBL; U44024; AAA93305.1;
MGD; MGI:95560; Flt31.;
InterPro; IPR00123; Flt3_lig.
InterPro; IPR001230; Prenyl_site.
Pfam; PF02947; flt3_lig. 1.
PROSITE; PS00294; PRENYLATION; UNKNOWN_1.
                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.

MCClanahan T., Culpepper J., Campbell D., Wagner J., Franz-Bacon K.,

Matteson J., Tsai S., Luh J., Guimares M.J., Mattei M.-G., Rosnet O.,

Birnbaum D., Hannum C.;

"Flt3 ligand: expression, genomic organization, alternatively spliced
                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia;
                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=10090;
             61
                                      VAVNLQDEKHCKALWSLFLAQRWIEQLKTVAGSKMQTLLEDVNTEIHFVTSCTFQPLPEC
Similarity
                                                                                                                                             172 AA;
                                                                                            Conservative
                                                                                                                                             19465 MW;
                                                                                                       71.9%;
98.2%;
                                                                                          Score 879; DB 11; Length 172; Pred. No. 1.5e-81; 1; Mismatches 2; Indels
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                                                                                                                                            UNKNOWN_1.
04F0A010171E3384 CRC64;
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               120
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RESULT 2
Q8VCH
1D C04
C08VC
AC Q8VC
DT 01-M
DT 01-J
DT 01-J
DT 01-J
DT Simi
OS Mus
CC Euka
OC Mamm
OX NCBII
RN [1]
RN [1]
RN [1]
RR SEQU
RC TISS
RA Stra
Stra
RL Subm
DR Inte
DR Pina
CM Kina
SQ SEQU
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Submitted (DEC-2001) to the EMBL/GenBank/DDBJ
EMBL; BC019801; AAH19801.1; -
InterPro: IPR004213; Flt3_lig.
Pfam; PF02947; flt3_lig; 1.
                                                                                                                                                      Bos taurus (Bovine).
Bukaryota; Metazoa; Chordata; Craniat
Mammalia; Eutheria; Cetartiodactyla;
Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                Q9GKE0;
01-MAR-2001 (TrEMBLrel. 16,
01-MAR-2001 (TrEMBLrel. 16,
01-DEC-2001 (TrEMBLrel. 19,
             J. Immunol. 165:6966-6974(2000).
EMBL; AFF882985; AAF99322.1; -
InterPro; IPR004213; Flt3_lig.
Pin; PF02947; flt3_lig; 1.
                                                        MEDLINE=20570936; PubMed=11120823; Mwangi W., Brown W.C., Palmer G.H.; Mwangi W., Brown W.C., Palmer Green Tyrosine required for receptor binding and functiligand isoforms.";
   SEQUENCE
                                                                                                                                                                                                      01-DEC-2001 (TrEMBLrel. Flt3 ligand isoform-1.
                                                                                                                                                                                                                                                                Q9GKE0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; I
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation updat similar to FMS-like tyrosine kinase 3 ligand.
                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                             NCBI_TaxID=9913;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kinase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=10090;
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  ΑA;
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 32390 MW;
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Last annotation updat
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Pred. No. 7.7e-78;
0; Mismatches 4
                                                                                                                                                                 Craniata; Vertebrata; Euteleostomi; actyla; Ruminantia; Pecora; Bovoidea
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  D68B9ED79221202D CRC64;
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RESULT 4
Q8WNW1
ID .08WN
AC Q8WN
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DT 01-M
DT 01-J
DE F1t3
GN F1t3
GN F1t3
GN F1t3
GN F1t3
CO Mamm
OC Bovi
RN [1]
RP SEQUI
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DR Pfan
DR Pfan
TO RS Pfan
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Best Local
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Best Local
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01-MAR-2002 (TrEMBLrel. 2
01-UUN-2002 (TrEMBLrel. 2
01-UUN-2002 (TrEMBLrel. 2
Flt3 ligand.
FLT3 LIGAND.
                                                                                                                                                                                                                                                                                                                                                                              Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases EMBL; AB051841; BAB79634.1; -... IPR004213; F113_119. Pfam: PF02947; f1t3_119; 1...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea
                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                       Hikono H., Momotani E.;
"Cloning of a cDNA for bovine flt3 ligand.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bovidae; Bovinae;
NCBI_TaxID=9913;
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                                                          SLPGPQSPLLLLLLLLLPVALLLLATAWCLCRWRRRRTRYPGERRRTLRPRESSHLPA
                                                                                        ELPEPR-PRQLLLLLLLPLTLVLLAAAWGL-RWQRARRR---
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                              ----GELHPGVPLPSHP
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63.2%;
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62.8%;
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Last annotation update)
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                                                                                                                                                                                                                                                                                                      Pred. No. 1.2e-70;
Nismatches 4
                                                                                                                                                                                                                                                                                                                                     Score 774.5;
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Pred. No. 3.7e-71;
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RESULT
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Best Local
                   Yang S., Sim G.K.;
Yang S., Sim G.K.;
Yang S., Sim G.K.;
Yang S., Sim G.K.;

Molecular cloning of canine and feline flt3 ligand reveals high degree of similarity to the human and mouse homologue but unique long cytoplasmic domain.",
DNA Seq. 11:163-166(2000).
EMBL; AFI55149; AAF87089.1; -.
InterPro: IPR004213; Flt3_lig.
Pfam; PF02947; flt3_lig; 1.
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01-OCT-2000
01-JUN-2002
                                                                                                                                                                                                                                                                                        Q9MZU9
                                                                                                                                                                                  Felis silvestris catus (Cat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Carnivora; Fissipedia; Felidae;
                                                                                                                                                                                                                              01-JUN-2002
Flt3 ligand
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Mammalia; Eutheria; Carnivora; Fissipedia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OAZM60
                                                                                                                                    SEQUENCE FROM N.A.
MEDLINE=20358731; PubMed=10902925;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    degree of similarity to the human
long cytoplasmic domain.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Canis familiaris (Dog).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q9MZV0;
                                                                                                                                                                          NCBI_TaxID=9685;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MTVLAPAWSPNSSLLLLLLLLSPCLRGTPDCYFSHSPISSNFKVKFRELTDHLLKDYPVT 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         S., Sim G.K.;
                                                                                                                                                                                                                                                                                                                                                                                                 LREVQTNISHLLKDTCTQLLALKPCIGKACQNESRCLEVQCQPDSSTLLPPRSPIALEAT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VAVNLQDEKHCKALWSLFLAQRWIEQLKTVAGSKMQTLLEDVNTEIHFVTSCTFQPLPEC 120
                                                                                                                                                                                                                                                                                                                                                                           ELPEPR-PRQLLLLLLLLPLTLVLLAAAWGLRWQRARRRGELHPG 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                      VASNLQDDELCGAFWRLVLAQRWMVRLQAVAGSQMQILLEAVNTEIHFVTFCAFQPLPSC 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MIVLAPAWSPTAS-LLLLLLLSPGLRGTPDCSFSHSPISSTFAVTIRKLSDYLLQDYPVT 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AF155148; AAF87088.1; -.
Pro; IPR004213; Flt3_lig.
PF02947; flt3_lig; 1.
NCE 294 AA; 32394 MW;
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0 (TrEMBLrel. 15,
2 (TrEMBLrel. 21,
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70.2%;
 62.2%;
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Pred. No. 1.3e-70;
3; Mismatches 38
 Score
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 761;
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                                                                                                mouse homologue but uniquely
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 291;
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RESULT
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J. Immunol. 165:0900
EMBL; AF282986; AAF99323.1; -
InterPro: IPR004213; F1t3_1ig.
Pfam; PF02947; f1t3_1ig; 1.
Pfam; PF02947; f1t3_1ig; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Cetartioda Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-MAR-2001 (TrEMBLrel. 01-DEC-2001 (TrEMBLrel. Flt3 ligand isoform-2.
                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-20570936; PubMed=11120823; Mwangi W., Brown W.C., Palmer G.H.; Mwangi W., Brown W.C., Palmer G.H.; Indentification of fetal liver tyrosine required for receptor binding and functifications.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q9GKD9;
01-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q9GKD9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bos taurus (Bovine).
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                                                                                                                                                                                                                                                                                                        Local Similarity
mes 150; Conserv
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                                                                                                                ELPEPR-PRQLLLLLLLLPLTLVLLAAAWGL-RWQRARRR------
                                                                                                                                                                 LRFVQTNISHLLKDTCTQLLALKPCIGKACQNFSRCLEVQCQPDSSTLLPPRSPIALEAT
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                                                DTESELGGSQLEPG-PFLGHP
                                                                                                 SLPGPQSPLLLLLLLLLPVALLLLATAWCLCRWRRRRRTRYPGERRRTLRPRESSHLPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ALPAPQ-APLILLLLLLPVALLLMSAAWCLHWRRRRWR 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LREVQTNISHLLQDTSEQLAALKPWITR--RNESGCLELQCQPDSSTPLPPRSPRALEAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VASNLQDDELCGPFWHLVLAQRWMGRLKAVAGSQMQSLLEAVNTEIHFVTLCAFQPLPSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MIVLAPAWSPTTS-LLLLLLLSPGLRGSPDCSFSHSPISSTFKVTIRKLSDYLLQDYPVT
                                                                                                                                                                                                                                                                                                                                                                                                          165:6966-6974(2000).
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                                                                        -GELHPGVPLPSHP 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                  -DTHQQLEALKPWI - -THRNFSRCLELQCQPDSPTLLPPRSPGALGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chordata; Craniata;
Cetartiodactyla; Run
                                                                                                                                                                                                                                                                                                        55.5%; Score 678.5; DB 6 57.5%; Pred. No. 6.4e-61; tive 19; Mismatches 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               71.1%;
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19,
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                         725A7F77A95DA98B CRC64;
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ion using
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Best Local
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Bent A.F., Kunkel B.N., Dahlbeck D., Brown K.L.
Giraudat J., Leung J., Staskawicz B.J.;
"RPS2 of Arabidopsis thaliana: a leucine-rich
disease resistance genes.";
Science 265:1856-1860(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence up
01-JUN-2002 (TrEMBLrel. 21, Last annotation
RPS2 (Disease resistance protein RPS2).
RPS2 OR F20B18.200 OR AT4G26090.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bevan M., Rose M., Hempel S
Mayer K.F.X., Schueller C.;
Submitted (MAR-1999) to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=95007758; PubMed=7923358; Mindrinos M., Katagiri F., Yu G., Ausubel F.M.; "The A. thaliana disease resistance gene RPS2 encodes a protein containing a nucleotide-binding site and leucine-rich repeats.", Cell 78:1089-1099(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eurosids II; Brassicales; Brassicaceae; Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q42484
Q42484;
                                                                                                                                                                                                                                                                                                                                          EMBL;
                                                                                                                                                                                                                         PRINTS;
                                                                                                                                                                                                                                                                          InterPro; IPR000767;
InterPro; IPR001611;
                                                                                                                                                                                                                                                                                                                                                      EU Arabidopsis sequencing Submitted (MAR-2000) to the
                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. Rose M., Hempel S., Submitted (MAR-2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                          EU Arabidopsis sequencing project; Submitted (MAR-1999) to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Arabidopsis thaliana (Mouse-ear cress).
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                                                                                                                                                                                                                                                              InterPro; IPR002182;
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ELGFADLEYLENLTTLGITVLSLETLKTLFEFGALHKHIQHLHVEECNELLYFNLPSLTN
                                                   VLPQELGNLRKLKHLDLQRTQFLQTIPRDAICWLSKLEVLNLYYSYAGWELQSFGEDEAE
                                                                                                                               LLLLLLLSPCLRGTPDCYFSHSPISSNFKVKFRELTD-----HLLKDYPVTVA----
                                                                                                     LTTLMLQQNSSLKKIPTGFFMHMPVLRVLDLSFTSITEIPLSIKYLVELYHLSMSGTKIS
                                                                                                                                                                                                               PF00931; NB-ARC; 1.
S; PR00364; DISEASFPO
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U12860; AAA50236.1;
                                                                                                                                                          Similarity
55; Conser
                                                                             VNLQDEKHCKALWSLFL-----
                                                                                                                                                                                                            909 AA;
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A; 104640 MW;
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                                                                                                                                                                  7.8%;
22.8%;
                                                                                                                                                                                                                                                                          Disease_resist.
                                                                                                                                                                                                                                                               NB-ARC
                        VTSCTFQPLPECLRF--VQTNISHLLKDTCTQLLALK-PCIGK 148
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                                                                                                                                                                                                                                                                                                                                                                    project;
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                                                                                                                                                       Score 95.5; DB Pred. No. 0.52; 0; Mismatches
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                                                                           -AQRWIEQLKTV----
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RESULT

1D 9665

1D 9665

AC 99

PT 01

PT 0
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TISSUE-FRONTAL LOBE LEFT; Osada N., Hida M., Kusuda J., Tanuma Suzuki Y., Sugano S., Hashimoto K.; "Isolation of full-length cDNA clones libraries.";
                                                                                                                                                                                                                                                         Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;

Cercopithecinae; Macaca.

NCBI_TaxID=9541;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q9BGY6;
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"NEDO human cDNA sequencing project.";
Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AKO26226; BAB15400.1:
EMBL; AKO26226; BAB15400.1:
SEQUENCE 355 AA; 37894 MW; 52C41A73E673623C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                         01-JUN-2001 (TrEMBLrel. 17, Cr
01-JUN-2001 (TrEMBLrel. 17, La
01-JUN-2002 (TrEMBLrel. 21, La
01-JUN-2002 (TrEMBLrel. 21, La
Hypothetical 56.5 kDa protein
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01-MAR-2001 (TYEMBLRel. 16, Last sequence up
01-DEC-2001 (TYEMBLRel. 19, Last annotation
CDNA: FLJ22573 fis, clone HSI02387.
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                                                                                                                                                                                    SEQUENCE FROM N.A
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Q9ASP5;
Q1-JUN-2001 (TrEMBLrel. 17, Created)
Q1-JUN-2001 (TrEMBLrel. 17, Last sequence update)
Q1-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Q1-JUN-2002 (TrEMBLrel. 17, Last sequence resistance protein RPS2
Q1-JUN-2001 (TrEMBLrel. 17, Last sequence update)
Q1-JUN-2002 (Tr
                                       Pfam; PF00560; LRR; 4.
Pfam; PF00951; NB-ARC; 1.
PRINTS; PR00364; DISEASERSIST
SMART; SM00382; AAA; 1.
SMART; SM00370; LRR; 4.
                                                                                                                                                                            Genetics 158.439-450(2001).
EMBL; AF368301; AAK,ATPASE.
InterPro; IPR003593; AAA_ATPASE.
InterPro; IPR000767; Disease_resist.
InterPro; IPR001611; LRR.
InterPro; IPR003592; LRR.out.
InterPro; IPR003592; LRR.out.
                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
MEDLINE=21231631; PubMed=11333251;
Banerjee D., Zhang X., Bent A.F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR001611; LRR.
InterPro; IPR000483; LRR_Cterm.
InterPro; IPR003592; LRR_out.
InterPro; IPR003591; LRR_typ.
pfam; PF00560; LRR; 6.
Pfam; PF01463; LRRCT; 1.
                                                                                                                                                                                                                                                                                                                        between RPS2 and other host factors disease resistance.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hypothetical protein SEQUENCE 510 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRINTS; PR00019; LEURICHRPT. SMART; SM00370; LRR; 4. SMART; SM00369; LRR_TYP; 6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q9ASP5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted
                        ATP-binding
                                                                                                                                                                InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                     "The leucine-rich repeat domain can
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                223
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LSNNFISYIGKDAFRPLPQ-LQEVDLSRNRLAHMPDVFTPLKQLIHLSLDKNQWSCTCDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SKLHSLQVLVLSNNALRTLRGSWFRNTRGLTRLQLDGNQITNLTDSSFGGTNLHSLRHLD 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           --LKDYPVTVAVN-----LQDE--KHCKALWSLFLAQRWIEQL--KTVAGSKMQTL--LE 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STNLSLLFNLALLSLSRNGIEDVQEDALDGLTMLRTLLLEHNQISSS-----SLTDHTF 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RSPLLPGQDVALLTVLGFAGAVGLTCLGLVVFNWKLQQGKANEH 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HPLARELRNY IKSSAHTLRNAKDLNCQPSTAAVAAAQSVLRLSETNCDPKAPNFTLVLKD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -LLLLP-----LTLVLLAAAWGL-----RWQRARRRGELH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ----ALKPCIGKACQNFSRCLEVQCQPDSSTLLPPRSPIALEATELPEPRPRQLLLL--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    tted (FEB-2001)
AB055271; BAB21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity 23.9
68; Conservative
                                                                                                                                                           IPR002182; NB-ARC.
    909
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              510 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
    ΑA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2001) to the EMBL/GenBank/DDBJ databases. BAB21895.1; ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 56496 MW;
    104613
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    WW.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 93.5; DB
Pred. No. 0.43;
34; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FF52698C2F9119E8 CRC64;
  F83E0F881B409DFA CRC64;
                                                                                                                                                                                                                                                                                                                                            determine effective interaction in Arabidopsis RPS2-mediated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         909
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Embryophyta; Tracheophyta; edons; core eudicots; Rosid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -----ISHLLKD----TCTQLL 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ΑĀ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   105;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 510;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   77;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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RESULT 12
Q83443
ID Q8344
RESULT 13
Q83448
ID 08344
AC Q8344
AC 01-NO
DT 01-NO
DT 01-MA
DE VP7.
OS MURIN
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                                                                                                                                                                                                                                                   MEDIINE=94330134; PubMed=8053149; Dunn S.J., Burns J.W., Cross T.L., Vo Greenberg H.B.; Greenberg H.B.; "Comparison of VP4 and VP7 of five mu Virology 203:250-259(1994).
EMBL; U08422; AAA50485.1; -.
InterPro; IPR001963; VP7.
Pfam; PF000434; VP7; 1.
ProDom; PD000191; VP7; 1.
ProDom; PD000191; VP7; 1.
SEQUENCE 326 AA; 36990 MW; B579E9
                    Q83448;
Q83448;
Q1-NOV-1996
Q1-NOV-1996
Q1-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q83443;
Q83443;
Q1-NOV-1996
Q1-NOV-1996
Murine rotavirus
                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=28327;
                                                                                                                                                                                                                                                                                                                                                                                                             Viruses;
                                                                                                                                                                                                                                                                                                                                                                                                                      Murine rotavirus
                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                   STRAIN-EC
                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             149
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14 LLLLLLLSPCLRGTPDCYFSHSPISSNFKVKFRELTD------HLLKDYPVTVA----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                                      92
                                                                                                                                          64
                                                                                                                                                                38
                                                                                                                                                                                       15 LLLLLLSPCLR-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACQNFSRCLEVQCQPDSSTLLPPRSPIALEATELPEPRPRQLLLLLLLLPLTLVLLAAAW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LTTLMLQQNSYLKKIPTGFFMHMPVLRVLDLSFTSITEIPLSIKYLVELYHLSMSGTKIS
                                                                                                                      EMNDNSWKDTLSQLFLTKGW
                                                                                                                                           NLQDEKHCKALWSLFLAQRW
                                                                                                                                                                LLVILILSPCIKAQNYGINLPITGSMDTAYANSTQSDTF-----LTSTLCLYYPTEAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EIHF-------VTSCTFQPLPECLRF--VQTNISHLLKDTCTQLLALK-PCIGK 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VLPQELGNLRKLKHLDLQRTQFLQTIPRDAICWLSKLEVLNLYYSYAGWGLQSFQEDEVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ELGFADLEYLENLTTLGITVLSLETLKTLFEFGALHKHIQHLHVEECNDLLYFNLPSLTN
                                                                                                                                                                                                           24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               763
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   209
                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                           dsRNA viruses;
                    (TrEMBLrel.) (TrEMBLrel.)
                                                                                                                                                                                                                                                                                                                                                                                                                                           (TrEMBLrel.)
(TrEMBLrel.)
                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7.4%; 22.8%;
                                                                                                                                                                                                                     7.2%;
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20,
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                                                                                                                      111
                                                                                                                                           83
                                                                                                                                                                                                           11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     38; Mismatches
                    Created)
Last sequence update)
Last annotation updat
                                                                                                                                                                                      -GTPDCYFSHSPISSNFKVKFRELTDHLLKDYPVTVAV 63
                                                                                                                                                                                                                                                                                                                                                                                                                                           Created)
Last sequence update)
Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 90.5; D
Pred. No. 1.7;
                                                                                                                                                                                                                     Score 88.5; DB 12; Pred. No. 0.84;
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                                                                                                                                                                                                                                                       B579E98A10DCF8A6 CRC64;
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                                                                                                                                                                                                                                                                                                                                          Vo P.T.,
                                                                                                                                                                                                                                                                                                                        murine
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                                                                 326
                                                                 B
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                                                                                                                                                                                                                                                                                                                        rotavirus
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                                                                                                                                                                                                                                                                                                                                             Bremont M.,
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                                                                                                                                                                                                                                326;
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Best Local S
Matches 24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR001963; VP7. Pfam; PF00434; VP7; 1. ProDom; PD000191; VP7; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Greenberg H.B.;
"Comparison of VP4 and VP7 of Virology 203:250-259(1994).
EMBL; U08427; AAA50490.1; -.
                                                                                                                                                                                                                       SMART; SM00409; IG; 1.
SMART; SM00410; IG_like; 1.
SMO0410; IG_like; 1.
                                                                                                                                                                                                                                                                                                  Tracey A.; submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases EMBL; AL136967; CAC09453.1; .
                                                                                                                                                                                                                                                                                                                                                                                                           01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DJ149M18.1.1 (natural killer cell p44-related gene 1 (NKp44RG1)).
DJ149M18.1. (NATURAL KILLER)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=94330134;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=28327;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Viruses; dsRNA viruses; Reoviridae; Rotavirus
                                                                                                                                                                                                                                                                       InterPro;
InterPro;
                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens (Human).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q9н563
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q9H563;
                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                             InterPro;
                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=9606;
152 NFSRCLEVQCQPDSSTLLP-PRSPIALEATELPEPRPRQLLLLLLLLLLPLTLVLLAAAWGL
                                                            112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14
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                                     107
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                                                                                   49
                                                                                                         64
                                                                                                                                                                                         Local
                                                                                                                               N
                                                                                                                                                                                                                                  T; SM00409; TG.

T; SM00409; TG.

T; SM00409; TG.

T; SM00409; TG.
                                                                                                                                                       7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LLLLLLSPCLR-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMNDNSWKDTLSQLFLTKGW 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NLQDEKHCKALWSLFLAQRW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LLVILILSPCIKAQNYGINLPITGSMDTAYANSTQSETF----
                                     YWCRIYRPSDNSVSKSVRFYLVVSPASASTQTSWTPRDLVSSQTQTQSCVPPTAGARQAP
                                                          --C-TFQP----LPECLRF------VQTNISHLLKDTCTQLLALKPCI-----GKACQ
                                                                                   -YEKKGWCKEA-SALVCIRLVTSSKPRTMAWTSRFTIWDDPDAGFFTVTMTDLREEDSGH
                                                                                                        NLQDEKHCKALWSLFLAQRWIEQLK--TVAGSKMQTLLEDVNTEIHFVTS------
                                                                                                                                                      AWSPNSSLLLLLLLLSPCLRGTPDCYFSHSPISSNFKVKFRELTDHLLK---DYPVTVAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Burns J.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  326 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PubMed=8053149;
J.W., Cross T.L.,
                                                                                                                                                                       7.2%; 5cc
23.8%; Pre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   36978 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -GTPDCYFSHSPISSNFKVKFRELTDHLLKDYPVTVAV 63
                                                                                                                                                                              Score 88; DB 4; Length 258; Pred. No. 0.73; 1; Mismatches 105; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No. 0.8
l; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 88.5; DB Pred No. 0.84;
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                                                                                                                                                                                                                           F21D9055BCA5DF0F CRC64
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                                                                                                                                 -FPGSQAQSKAQV-LQSVAGQTLTVRCQYPPTGSL
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01-MAY-1999 (TrEMBLrel.
01-MAR-2002 (TrEMBLrel.
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Eukaryota; Metazoa; (
Mammalia; Eutheria; I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nagase T., Ishikawa K., Suyama M., Kikuno R., Miyajima N., Tanaka A Kotani H., Nomura N., Ohara O.; "Prediction of the coding sequences of unidentified human genes. XI The complete sequences of 100 new cDNA clones from brain which code for large proteins in vitro.";
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InterPro; IPR000194; ATPASE_a/bcentre.
PROSITE; PS00152; ATPASE_ALPHA_BETA; UNKNOWN_1.
SEQUENCE 765 AA; 86915 MW; EICCAF0771A9E9F9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE=BRAIN;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GVPD-----NIKSTYKV-----NHIWKFRYDRPFHKGTK-DKENEFKSLWVERTSLYL 282
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                                                                                                                 TRVIPRRSPLSYPA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AQ-----RW--IEQLKTVAGSKMQT---LLEDVNTEIH-FVTSC-----TFQPLPECL 121
                                                                                                                                                STLLPPRSPIALEA 179
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8 secs
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N., Ohara O.;
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                                                                                                                 474
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                                  24,
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20,
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Last annotation updat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 4;
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GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
```

OM protein - protein search, using sw model

Run on: November 24, 2002, 10:02:26; Search time 31.2296 Seconds (without alignments) 985.632 Million cell updates/sec

Title: US-09-448-378-2 1223

Perfect score:

Sequence: 1 MTVLAPAWSPNSSLLLLLLLL......WQRARRRGELHPGVPLPSHP 231

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters:

Minimum DB Maximum DB seq length: 0
seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database : A\_Geneseq\_101002:\*
1: /SIDS2/gcgdata/gcgdsta/g

/SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1989.DAT: \*
/SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1989.DAT: \*
/SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1990.DAT: \*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

10	9	8	7	6	5	4	ω	ر د	<u></u>	No.	Result
879	879	879	1004	1006	1208.5	1212.5	1223	1223	1223	Score	
71.9	71.9	71.9	82.1	82.3	98.8	99.1	100.0	100.0	100.0	Match L	Query
220	220	172	189	288	232	232	231	231	231	Length DB	
22	22	22	22	22	22	16	22	20	16	BB	
AAB20190	AAB20188	AAB20191	AAB20187	AAU02129	AAB20189	AAR66177	AAB20186	AAW67768	AAR67540	ID	
Mouse Flt-3 ligand	Mouse Flt-3 ligand	Mouse Flt-3 ligand	Mouse Flt-3 ligand	Flt-3 ligand (FL)	Mouse Flt-3 ligand	Mouse MoT110/T118	Mouse Flt-3 ligand	Murine flt3-ligand	Mouse flt-3 ligand	Description	

45	4 4	4 2	41	40	39	38	37	36	35	34	ω ω	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	11
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#### ALIGNMENTS

RESULT 1
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ID AAR67540
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AC AAR6
XX MOUS
XX MOUS
XX MUS
XX HEY
FT Pept
FT Doma
FT Doma 24-MAY-1993; 12-AUG-1993; 25-AUG-1993; Flt-3 ligand; flt3-L; anemia; cancer; AIDS; gene therapy Mouse flt-3 ligand. 05-AUG-1995 AAR67540; AAR67540 standard; Protein; Domain Mus sp. 19-MAY-1994; 07-DEC-1994. Domain Domain Peptide EP627487-A. (first entry) 93US-0068394. 93US-0106463. 93US-0111758. 94EP-0303575 /label= Sig\_peptide 28..188 Location/Qualifiers
1..27 189..211 /label= Transmembrane\_domain /label= Cytoplasmic\_domain label = Extracellular\_domain 231 AΑ

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RESULT 2
AAW67768
ID AAW6
XX
AC AAW(
XX 25-1
XX 25-1
XX Ant
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07-MAR-1994;
11-MAY-1994;
           Abbott NM,
                                                       17-JUN-1997;
                                                                           12-JUN-1998;
                                                                                                  23-DEC-1998
                                                                                                                       W09857655-A1
                                                                                                                                                              Antigen-specific peripheral immune tolerance; flt3-ligand; flt3-L; immunogenic; autòimmune disease; organ transplantation; food aller tissue transplantation.
                                                                                                                                                                                                                               25-MAR-1999
                                                                                                                                                                                                                                                                         AAW67768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cDNA encoding mouse flt3-ligand (flt3-L) was isolated from a cDNA library of T-cell line P7B-0.3A4 in CV-1/EBNA-1 cells using a slide autoradiography method. Flt3-L stimulates production of progenitor and stem cells, and can be used e.g.
                                                                                                                                                                                                         Murine flt3-ligand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Page 25-27; 33pp; English.
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                        (IMMV ) IMMUNEX CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB;
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                                                                                                                                                                                                                                                                                                                                                                                 LREVQTNISHLLKDTCTQLLALKPCIGKACQNFSRCLEVQCQPDSSTLLPPRSPIALEAT
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DB; AAQ79076.
                                                                                                                                                                                                                                                                                                                             ELPEPRPRQLLLLLLLPLTLVLLAAAWGLRWQRARRRGELHPGVPLPSHP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 231 AA;
            Mowat AM,
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                                                   97US-0877421
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94US-0209502.
94US-0243545.
                                                                           98WO-US12085
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             Viney JL;
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Pred. No. 5.2e-115;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A method has been developed of initiating or enhancing: (i) an antigen-
CC specific immune tolerance; or (ii) immunotolerance of a therapeutic
CI immunogenic molecule by addition of a polypeptide, before, after or with
CC the mucosal administration of an immunotolerising amount of the antigen
CC or therapeutic molecule, respectively. The polypeptide is capable of
CD binding the filt3 receptor and is: a) amino acids 28 x of murine filt3
CC ligand (filt3-L), where x is an amino acid between 163-231; b) amino
CC acids 28 y of human filt3-L, where y is an amino acid between 160-235;
CC and C) a polypeptide that has at least 90% identity to the polypeptides
CC of either (a) or (b). The method ameliorates the effects of autoimmune
CC diseases, food allergies or organ or tissue rejection following
CC transplantation. Administration of filt3-L allows lower doses of antigens
CC to be used in vivo for mucosally administered antigens. The present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches 231;
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                                                                                                                                                                                                                                                                                                                                                                Flt-3 ligand; Fms-like tyrosine kinase; mouse; vaccine;
immunotherapy; therapy; tumour; cancer; melanoma; glioma;
lymphoma; autoimmune disease; infection; gene therapy.
                         Domain
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N-PSDB;
                                                                         Domain
                                                                                                                                 Domain
                                                                                                                                                                                    Protein
                                                                                                                                                                                                                                         Peptide
                                                                                                                                                                                                                                                                                                                        Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mouse Flt-3 ligand
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DB; AAV81505.
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                                                                                                                                                                                    /label=
28..231
                      /label= Transmembrane_domain 212...231
                                                                                                                              /label=
28..188
                                                                              189.
                                                                                                                                                                                                                                                                   Location/Qualifiers
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Pred. No. 5.2e-115;
Mismatches 0;
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RESULT 4
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   compositions comprising the polynucleotides are useful for suppressing tumour growth in a mammal. The tumour is melanoma, glioma or lymphoma, particularly B-cell lymphoma. They can also be used for the prophylactic and/or therapeutic treatment of:
(a) bacterial (e.g. Bacillus infections), viral (e.g. hepatitis E and C in humans), parasitic (e.g. malaria) and fungal infections;
(b) autoimmune diseases (e.g. rheumatoid arthritis and osteoarthritis); (c) cancer; and (d) Aujeszky's disease in pigs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     polynucleotide may encode the present full-length murine Flt 3 ligand polypeptide, or amino acids 28-163, 1-163, 28-189 or 1-189 of the Flt-3 ligand. The polynucleotides are incorporated into the cells of the vertebrate in vivo, and a prophylactically or therapeutically effective amount of Flt-3 ligand and 1 or more antigens or cytokines is produced in vivo. Pharmaceutical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          administering in vivo, into a tissue of a vertebrate, a Flt-3 ligand-encoding polynucleotide, and 1 or more antigen- or cytokine-encoding polynucleotides. The Flt-3 ligand-encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Immunogenic compositions comprising Flt-3 ligand encoding polynucleotide and one or more antigen, or cytokine encoding polynucleotides, useful for suppressing timour growth and for treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 2; Page 120; 149pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            autoimmune diseases (e.g. rheumatoid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30-JUL-1999;
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               AAR66177 standard; Peptide; 232
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                                                                                                                                   ELPEPRPROLLLILLILTIVILIAAAWGIRWQRARRRGELHPGVPLPSHP 231
                                                                                                                                                                                                                                   VAVNLQDEKHCKALWSLFLAQRWIEQLKTVAGSKMQTLLEDVNTEIHFVTSCTFQPLPEC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     other examples of these diseases are given in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ရှေ
                                                                                                                                                                                                                                                                                                                                                                                                                                        231 AA;
                                                                                                                                                                                                                                                                                                                                                                       Conservative
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                                                                                                                                                                                                                                                                                                                                                                                     100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               is that of mouse Fms-like tyrosine kinase
                                                                                                                                                                                                                                                                                                                                                                     0;
                                                                                                                                                                                                                                                                                                                                                                                     Score 1223; DB 22; Pred. No. 5.2e-115;
                                                                                                                                                                                                                                                                                                                                                                       Mismatches
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13-AUG-1993;
24-AUG-1993;
19-NOV-1993;
03-DEC-1993;
                                                                                                                                                                                                                                                                                                                                                         A cDNA library from the human stromal cell line 29SV48, in pME18S, was screened with an 800 bp fragment derived from mouse clone T118. This fragment encompasses the coding region conserved between two mouse clones, T118 and T110. Approx. 20 positive clones were selected and partially sequenced. Two clones, S86 and S109, were found to be approx. 75% homologous to the mouse clones over the first 163 AAs. Clone S86 continued to show homology to T110 until the stop codon, although to a lesser degree, for an overall homology of 66%. Clones T118 and clone to the beautiful the stop codon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (INRM )
                                                                                                                                                                                                                                                                                                    $109 do not show homology to each other or to the other clones after mouse residue 163 (human residue 160). An additiona mouse clone designated MBB has a 29 AA insert at the junction between the common and divergent portions of the mouse ligand.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 11; page 79-80;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New ligand for the Flt3 tyrosine kinase receptor - and related nucleic acid, vectors, host cells and antibodies, useful for treating abnormal cell physiology and proliferation, e.g. cance also for diagnosis and drug screening
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Birnbaum D,
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07-JUL-1993;
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DB; AAQ79464.
ELPEPRPRQ-LLLLLLLLPLTLVLLAAAWGLRWQRARRRGELHPGVPLPSHP
                                                                                                                                                                          MTVLAPAWSPNSSLLLLLLLLSPCLRGTPDCYFSHSPISSNFKVKFRELTDHLLKDYPVT
                                                         LRFVQTNISHLLKDTCTQLLALKPCIGKACQNFSRCLEVQCQPDSSTLLPPRSPIALEAT
                                                                                                                 VAVNLQDEKHCKALWSLFLAQRWIEQLKTVAGSKMQTLLEDVNTEIHFVTSCTFQPLPEC
                                                                                                                                                           MTVLAPAWSPNSSLLLLLLLLSPCLRGTPDCYFSHSPISSNFKVKFRELTDHLLKDYPVT
                                           LRFVQTNISHLLKDTCTQLLALKPCIGKACQNFSRCLEVQCQPDSSTLLPPRSPIALEAT
                                                                                                   VAVNLQDEKHCKALWSLFLAQRWIEQLKTVAGSKMQTLLEDVNTEIHFVTSCTFQPLPEC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INST NAT SANTE & RECH MEDICALE SCHERING CORP.
                                                                                                                                                                                                                                                                            232 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Culpepper
                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            93US-0112391.
93US-0155111.
93US-0162413.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      93US-0092549.
93US-0106340.
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93US-0089263.
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                                                                                                                                                                                                                             99.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         90pp; English.
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                                                                                                                                                                                                                  0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hannum CH,
                                                                                                                                                                                                                  Score 1212.5; DB Pred. No. 6e-114; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   proliferation, e.g. cancer
                                                                                                                                                                                                                                               DB 16;
                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                                                 Length
                                                                                                                                                                                                                                                 232;
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                                                                                                                                                                                                                    Gaps
                                                                                                    120
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181

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RESULT 5
AAB20189
ID AAB2
    be used for the prophylactic and/or therapeutic treatment of:

(a) bacterial (e.g. Bacillus infections), viral (e.g. hepatitis and C in humans), parasitic (e.g. malaria) and fungal infections (b) autoimmune diseases (e.g. rheumatoid arthritis and osteoarthritis); (c) cancer; and (d) Aujeszky's disease in pigs.
                                                                                   antigens or cytokines is produced in vivo. Pharmaceutical compositions comprising the polynucleotides are useful for suppressing tumour growth in a mammal. The tumour is melanoma glioma or lymphoma, particularly B-cell lymphoma. They can al
                                                                                                                                                                                                           administering in vivo, into a tissue of a vertebrate, a Flt-3 ligand-encoding polynucleotide, and 1 or more antigen- or cytokine-encoding polynucleotides. The Flt-3 ligand-encoding
                                                                                                                                            the cells of the vertebrate in vivo, and a prophylactically or therapeutically effective amount of Flt-3 ligand and 1 or more
                                                                                                                                                                             polynucleotide may encode the present sequence or the mature polypeptide. The polynucleotides are incorporated into
                                                                                                                                                                                                                                                                                                                                              Immunogenic compositions comprising Flt-3 ligand encoding polynucleotide and one or more antigen, or cytokine encoding polynucleotides, useful for suppressing tumour growth and for treating autoimmune diseases (e.g. rheumatoid arthritis) -
                                                                                                                                                                                                                                                         immune response of a vertebrate to an antigen or a cytokine by
                                                                                                                                                                                                                                                                             (Flt-3 ligand).
                                                                                                                                                                                                                                                                                                                      Claim 2; Page 125-126; 149pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB; AAF30307
                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2001-123319/13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       31-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       08-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Flt-3 ligand; Fms-like tyrosine kinase; mouse; vaccine; immunotherapy; therapy; tumour; cancer; melanoma; glion lymphoma; autoimmune disease; infection; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (VICA-) VICAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Domain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14-MAY-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAB20189
                                                                                                                                                                                                                                                                      present sequence is that of mouse Fms-like tyrosine kinase t-3 ligand). The invention is directed to enhancing the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ELPEPRPRQLLLLLLLLLTTLVLLAAAWGLRWQRARRRGELHPGVPLPSHP 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2000WO-US20679
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99US-0146170
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213..232
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28..232
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of these
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                                        infections;
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RESULT 6
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                                                                                                                                    New chimeric polypeptide, useful as anti-tumour vaccines, comprises carboxy terminal fragment of heat shock protein, Flt-3 ligand or cytoplasmic translocation domain of Pseudomonas exotoxin A and antigenic polypeptide -
                                                                                                                                                                                           WPI;
                                                                                                              Claim 9;
                                                                                                                                                                                                                                                           20-OCT-1999;
09-FEB-2000;
                                                                                                                                   antigenic
                                                                                                                                                                                                                 Wu T,
                                                                                                                                                                                                                                                                                                                                                               Unidentified.
                                                                                                                                                                                                                                                                                                                                                                                ETA dII; antigenic; imm vaccine; immunotherapy.
                                                                                                                                                                                                                                                                                                                                                                                            Mouse; granulocyte-macrophage-colony stimulating factor; GM chimeric; heat shock protein; HSP; Flt-3 ligand; FL; exotox ETA dII; antigenic; immunogenic; cytotoxic T cell response;
                                                                                                                                                                                                                                      (UYJO ) UNIV JOHNS HOPKINS SCHOOL MEDICINE
                                                                                                                                                                                                                                                                                            20-OCT-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                         Flt-3 ligand
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAU02129 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   specification.
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                                                                                                                                                                                          2001-290921/30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ELPEPRPRQ-LLLLLLLLLLLVLLAAAWGLRWQRARRRGELHPGVPLPSHP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LRFVQTNISHLLKDTCTQLLALKPCIGKACQNFSRCLEVQCQPDSSTLLPPRSPIALEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VAVNLQDEKHCKALWSLFLAQRWIEQLKTVAGSKMQTLLEDVNTEIHFVTSCTFQPLPEC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VAVNLQDEKHCKALWSLFLAQRWIEQLKTVAGSKMQTLLEDVNTEIHFVTSCTFQPLPEC
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                                                                                                          Fig 19; 110pp; English.
                                                                                                                                  polypeptide
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                                                                                                                                                                                                                                                           99US-0421608
2000US-0501097
                                                                                                                                                                                                                                                                                                                                                                                                                                         (FL) used to
                                                                                                                                                                                                                                                                                            2000WO-US41422
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         98.8%;
99.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                         make
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 1208.5;
Pred. No. 1.5
                                                                                                                                                                                                                                                                                                                                                                                                                                      chimeric immunogenic polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5e-113;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB
                                                                                                                                                                                                                                                                                                                                                                                                       factor; GM-CSF;
FL; exotoxin A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
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used in construction of a chimeric polypeptide comprising: (a) a first polypeptide domain containing a carboxy terminal fragment of a heat shoc protein (HSP), an FIt-3 ligand (FL), a cytoplasmic translocation domain of a Pseudomonas exotoxin A (ETA dII), or a granulocyte-macrophage color stimulating factor (GM-CSF); and (b) a second polypeptide domain containing an antigenic polypeptide. A composition comprising the chimeric polypeptide is useful for inducing an immune response such as a containing an antigenic polypeptide.

a heat shock

colony

The sequence represents the amino acid sequence of Flt-3 ligand (FL)

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QΥ
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Best Local S
Matches 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chimeric polypeptide present in the composition is administered as naked DNA by gene gun or equivalent, or by liposomal formulation. These are thus useful for vaccinating a mammal against infection by inducing an immune response to a pathogen. Preferably they are useful for vaccinating a mammal against a tumour antigen. The compositions and methods are useful for stimulating or enhancing the immunogenicity of a selected antigen or stimulating or enhancing a cellular immune response specific for that antigen. The chimeric nucleic acid molecules and vaccination methods, yield potent antigen-specific immunotherapy. The polynucleotides and DNA vaccines can induce a cellular immune response that is at least 40 fold more potent than conventional DNA vaccines. The vaccines are safe and useful for administration to domesticated or agricultural animals, as well as humans, and have low immunogenicity.
                                                                                                                                                                                                                                                                                                                                           Flt-3 ligand; Fms-like tyrosine kinase; mouse; vaccine;
immunotherapy; therapy; tumour; cancer; melanoma; glion
lymphoma; autoimmune disease; infection; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAB20187 standard; Protein; 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
WPI; 2001-123319/13.
N-PSDB; AAF30305, AA
                                                                                                                                 31-JUL-2000; 2000WO-US20679
                                                                                                                                                               08-FEB-2001.
                                                                                                                                                                                            WO200109303-A2
                                                                                                                                                                                                                                       Protein
                                                                                                                                                                                                                                                                                                                 Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                       Mouse Flt-3 ligand (secreted form).
                                                                                                                                                                                                                                                                                                                                                                                                                                  14-MAY-2001 (first entry)
                                            Hermanson GG
                                                                                                                                                                                                                                                                      Peptide
                                                                       (VICA-) VICAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MTVLAPAWSPNSSLLLLLLLLSPCLRGTPDCYFSHSPISSNFKVKFRELTDHLLKDYPVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ELPEPRPRQM 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ELPEPRPRQL 190
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VAVNLQDEKHCKALWSLFLAQRWIEQLKTVAGSKMQTLLEDVNTEIHFVTSCTFQPLPEC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VAVNLQDEKHCKALWSLFLAQRWIEQLKTVAGSKMQTLLEDVNTEIHFVTSCTFQPLPEC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               189;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       288 AA;
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                                                                           INC
                                                                                                      99US-0146170
                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                      /label= Signal_peptide
28..189
/label= Mature_protein
AAF30313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          82.3%;
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Pred. No. 5.3e-93;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
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                                                                                                                                                                                                                                                                                                                                                            glioma;
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immune response of a vertebrate to an antigen or a cytokine by administering in vivo, into a tissue of a vertebrate, a Pit-3 ligand-encoding polynucleotide, such as VR6200, and 1 or more antigen- or cytokine-encoding polynucleotides. The polynucleotides are incorporated into the cells of the vertebrate in vivo, and a prophylactically or therapeutically effective amount of Pit-3 ligand and 1 or more antigens or cytokines is produced in vivo. Pharmaceutical compositions comprising the polynucleotides are useful for suppressing tumour growth in a mammal. The tumour is melanoma, gliona or lymphoma, particularly B-cell lymphoma. The co-injection of VR6200 and tumour-specific antigen-encoding plasmid vR1623 into mice significantly enhanced protection from tumour challenge. The claimed pharmaceutical compositions can also be used for the prophylactic and/or therapeutic treatment of:

(a) bacterial (e.g. Bacillus infections), viral (e.g. hepatitis B and C in humans), parasitic (e.g. malaria) and fungal infections; (b) autoimmune diseases (e.g. rheumatoid arthritis and osteoarthritis); (c) cancer; and (d) Aujeszky's disease in pigs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present sequence is that of a secreted form of mouse Fms-li tyrosine kinase (Flt-3 ligand), lacking the transmembrane and cytoplasmic domains of the full-length form (see AAB20186). Th secreted form of the Flt-3 ligand is expressed by vector VR6200 (see AAF30313). The invention is directed to enhancing the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Immunogenic compositions comprising Flt-3 ligand encoding polynuclectide and one or more antigen, or cytokine encoding polynucleotides, useful for suppressing tumour growth and for treating autoimmune diseases (e.g. rheumatoid arthritis) -
                                                                             Various other examples of these diseases are given in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Page 121; 149pp; English.
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Sequence 189 AA;

0

specification.

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                                                                                                                                                                                                                Matches 189;
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  181
                           181
                                                    121
                                                                              121
                                                                                                                                 61
                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                            \vdash
                                                                                                                                                                                      1 MTVLAPAWSPNSSLLLLLLLLLSPCLRGTPDCYFSHSPISSNFKVKFRELTDHLLKDYPVT 60
1 ELPEPRPRQ 189
|||||||||
1 ELPEPRPRQ 189
                                                                   LRFVQTNISHLLKDTCTQLLALKPCIGKACQNESRCLEVQCQPDSSTLLPPRSPIALEAT 180
                                                                                                                       VAVNLQDEKHCKALWSLFLAQRWIEQLKTVAGSKMQTLLEDVNTEIHFVTSCTFQPLPEC 120
                                                                                                         VAVNLQDEKHCKALWSLFLAQRWIEQLKTVAGSKMQTLLEDVNTEIHFVTSCTFQPLPEC
                                                                                                                                                            LRFVQTNISHLLKDTCTQLLALKPCIGKACQNFSRCLEVQCQPDSSTLLPPRSPIALEAT 180
                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                             82.1%;
100.0%;
                                                                                                                                                                                                                0; Mismatches
                                                                                                                                                                                                                             Score 1004; DB 22;
Pred. No. 4.8e-93;
                                                                                                                                                                                                                                        Length 189;
                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                0
                                                                                                                                                                                                              Gaps
                                                                                                         120
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RESULT 8
AAB20191
ID AAB2
14-MAY-2001 (first entry)
                                                    AAB20191;
                                                             AAB20191 standard; Protein; 172
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Flt-3 ligand; Fms-like tyrosine kinase; mouse; vaccine; immunotherapy; therapy; tumour; cancer; melanoma; glioma; lymphoma; autoimmune disease; infection; gene therapy. Mus musculus Mouse Flt-3 ligand

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RESULT 9
AAB201887
ID AAB20
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Peptide
                                                                                                                                                                                                                                                                                                                                                                                                              antigens or cytokines is produced in vivo. Pharmaceutical compositions comprising the polynuclectides are useful for suppressing tumour growth in a mammal. The tumour is melanoma, glioma or lymphoma, particularly B-cell lymphoma. They can also be used for the prophylactic and/or therapeutic treatment of:

(a) bacterial (e.g. Bacillus infections), viral (e.g. hepatitis B and C in humans), parasitic (e.g. malaria) and fungal infections;

(b) autoimmune diseases (e.g. rheumatoid arthritis and osteoarthritis); (c) cancer; and (d) Aujeszky's disease in pigs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present sequence is that of mouse Fms-like tyrosine kinase (Flt-3 ligand). The invention is directed to enhancing the immune response of a vertebrate to an antigen or a cytokine by administering in vivo, into a tissue of a vertebrate, a Flt-3 ligand-encoding polynucleotide, and 1 or more antigen- or cytokine-encoding polynucleotides. The Flt-3 ligand-encoding cytokine-encoding polynucleotides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Immunogenic compositions comprising Flt-3 ligand encoding polynucleotide and one or more antigen, or cytokine encoding polynucleotides, useful for suppressing tumour growth and for treating autoimmune diseases (e.g. rheumatoid arthritis) -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2001-123319/13
N-PSDB; AAF30309.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               31-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               08-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200109303-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           polynucleotide may encode the present sequence or the mature polypeptide. The polynucleotides are incorporated into the cells of the vertebrate in vivo, and a prophylactically or therapeutically effective amount of Fit-3 ligand and lor more
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hermanson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (VICA-) VICAL
                                                                                                                                                                                                                                                                                                                                                    Sequence
                AAB20188 standard;
                                                                                                                                                                                                                                                                                                                                                                                    specification.
                                                                                                                                                                                                                                                                                                                                                                                                    Various other examples of these diseases are given in the
                                                                                               121
                                                                                                                                                                             61 VAVNLQDEKHCKALWSLFLAQRWIEQLKTVAGSKMQTLLEDVNTEIHFVTSCTFQPLPEC 120
                                                                                                                                                                                                                        Local Similarity
les 165; Conser
                                                                                              LRFVQTNISHLLKDTCTQLLALKPCIGKACQNFSRCLEVQCQPDRVSL 168
                                                                                                             LRFVQTNISHLLKDTCTQLLALKPCIGKACQNFSRCLEVQCQPDSSTL 168
                                                                                                                                                             VAVNLQDEKHCKALWSLFLAQRWIEQLKTVAGSKMQTLLEDVNTEIHFVTSCTFQPLPEC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Page 130; 149pp; English.
                                                                                                                                                                                                                                                                                                                                                        172 AA;
                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2000WO-US20679
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /label= Signal_peptide
28..172
/label= Mature_protein
                    Protein; 220
                                                                                                                                                                                                                                                                                                       71.9%;
98.2%;
                                                                                                                                                                                                                                                                                      Score
Pred.
1; Mis
                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                        e 879; DB 22;
. No. 1.7e-80;
ismatches 2;
                                                                                                                                                                                                                                                                                                                        Length 172;
                                                                                                                                                                                                                                                                                           Indels
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                                                                                                                                                                                                                                                                                           Gaps
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VAVNLQDEKHCKALWSLFLAQRWIEQLKTVAGSKMQTLLEDVNTEIHFVTSCTFQPLPEC 120

γ

61

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immune response of a vertebrate to an antigen or a cytokine by cadministering in vivo, into a tissue of a vertebrate, a Flt-3 ligand-encoding polynucleotide, and 1 or more antigen- or cytokine-encoding polynucleotides, and 1 or more antigen- or polynucleotide may encode the present sequence or the mature polynucleotide may encode the present sequence or the mature polynucleotide are incorporated into the cells of the vertebrate in vivo, and a prophylactically or therapeutically effective amount of Flt-3 ligand and 1 or more antigens or cytokines is produced in vivo. Pharmaceutical compositions comprising the polynucleotides are useful for suppressing tumour growth in a mammal. The tumour is melanoma, cylioma or lymphoma, particularly B-cell lymphoma. They can also be used for the prophylactic and/or therapeutic treatment of: (a) bacterial (e.g. Bacillus infections), viral (e.g. hepatitis B cand C in humans), parasitic (e.g. malaria) and fungal infections; (b) autolimnune diseases (e.g. rheumatoid arthritis and
Matches
                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Flt-3 ligand; Fms-like tyrosine kinase; mouse; vaccine;
immunotherapy; therapy; tumour; cancer; melanoma; glion
lymphoma; autoimmune disease; infection; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Immunogenic compositions comprising Flt-3 ligand encoding polynucleotide and one or more antigen, or cytokine encoding polynucleotides, useful for suppressing tumour growth and for treating autoimmune diseases (e.g. rheumatoid arthritis) -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2001-123319/13.
N-PSDB; AAF30306.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         31-JUL-2000; 2000WO-US20679
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mouse Flt-3 ligand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14-MAY-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                           The present sequence is that of mouse {\tt Fms-like} tyrosine kinase ({\tt Flt-3} ligand). The invention is directed to enhancing the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (VICA-) VICAL
                                                                                                                     (b) autoimmune diseases (e.g. rheumatoid arthritis and osteoarthritis); (c) cancer; and (d) Aujeszky's disease ivarious other examples of these diseases are given in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hermanson GG
                                                                  Sequence
                                                                                                   specification.
                  Local
al Similarity
177; Conserv
                                                                                                                   other examples
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Page 123-124; 149pp; English.
                                                                  220 AA;
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 Conservative
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28..220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /label= Mature_protein
                  71.9%;
Score 879; DB 22;
Pred. No. 2.4e-80;
5; Mismatches 21;
                                                                                                                                       disease in pigs
                                    Length 220;
   Indels
     12;
   Gaps
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RESULT 10
AAB20190
AX
AAB20190
AAB200
AX
AAB20190
AAB201
AAB20190
AAB201
AAB2
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Compositions of a vertebrate to an antigen or a cytokine by administering in vivo, into a tissue of a vertebrate, a Fit-3 control of the vertebrate, a fit-3 control of the vertebrate of a vertebrate, a Fit-3 control of the vertebrate of the verte
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Immunogenic compositions comprising Flt-3 ligand encoding polynuclectide and one or more antigen, or cytokine encoding polynuclectides, useful for suppressing tumour growth and for autoimmune diseases (e.g. rheumatoid arthritis).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  31-JUL-2000; 2000WO-US20679
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14-MAY-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hermanson GG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (VICA-)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LRFVQTNISHLLKDTCTQLLALKPCIGKACQNFSRCLEVQCQPDSSTLLPPRS----PIA 176
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DB; AAF30308.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2; Page 128; 149pp; English.
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28..220
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/label= Mature_protein
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Matches 177; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local :
Sequences AAY58204 and AAY58206-Y58209 resepctively represent encoded, mature, clone 1 and clone 19 canine Flt-3 ligand, while sequences AAY58210-Y58211 represent encoded and mature feline Flt-3 ligand. The invention relates to canine interleukin-4 (IL-4), canine or feline Flt-3 ligand, canine or feline CD40, canine or feline CD54 (CD40 ligand), canine IL-5, canine IL-13, feline interferon-alpha (IFN-alpha) and feline granulocyte macrophage colony stimulating factor (GMCSF), and nuclectides which encode these immunoregulatory proteins. The proteins, their associated nucleic acids, specific antibodies and inhibitors may be used as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         specification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (b) autoimmune diseases (e.g. rheumatoid arthritis and
osteoarthritis); (c) cancer; and (d) Aujeszky's disease in pigs.
Various other examples of these diseases are given in the
                                                                                                                                                                      Claim 3b; Page 159-160;
                                                                                                                                                                                                 Nucleic acids encoding useful for treating or
                                                                                                                                                                                                                                                                                           Sim G,
                                                                                                                                                                                                                                                                                                                                                                                                                                            WO9961618-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Canis familiaris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Canine Flt-3 ligand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14-MAR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAY58204;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAY58204 standard; Protein; 294
                                                                                                                                                                                                                                               N-PSDB;
                                                                                                                                                                                                                                                                                                                                                     29-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                                                 28-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                 02-DEC-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Flt-3 ligand; antibody; canine; feline; inhibitor; immune response;
                                                                                                                                                                                                                                                                                                                        (HESK-) HESKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      mmunoregulation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      178
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MTVLAPAWSPNSSLLLLLLLLSPCLRGTPDCYFSHSPISSNFKVKFRELTDHLLKDYPVT 60
                                                                                                                                                                                                                                             2000-072623/06
DB; AAZ55487, AAZ55488, AAZ55489, AAZ55490
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LREVQTNISHLLKDTCTQLLALKPCIGKACQNFSRCLEVQCQPDSSTLLPPRS----PIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VAVNLQDEKHCKALWSLFLAQRWIEQLKTVAGSKMQTLLEDVNTEIHFVTSCTFQPLPEC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VAVNLQDEKHCKALWSLFLAQRWIEQLKTVAGSKMQTLLEDVNTEIHFVTSCTFQPLPEC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LTATALLTVCPGLLLPLVGTSHMFFLPYFLSFLSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LEATELPEPRPRQLLLL-----LLLLPLTLVLLAA 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LRFVQTNISHLLKDTCTQLLALKPCIGKACQNFSRCLEVQCQPGNG---GPRAQHHGATR 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MTVLAPAWSPNSSLLLLLLLLSPCLRGTPDCYFSHSPISSNFKVKFRELTDHLLKDYPVT
                                                                                                                                                                                                                                                                                         Yang S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           220 AA;
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                                                                                                                                                                                                                                                                                                                          CORP
                                                                                                                                                                                                                                                                                                                                                     98US-0087306
                                                                                                                                                                                                                                                                                                                                                                                 99WO-US11942
                                                                                                                                                                                                                                                                                           Dreitz MJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        tumour; cancer; autoimmune disease; vaccine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              71.9%;
                                                                                                                                                                                                 immunoregulatory proteins from cats or dogs, preventing e.g. tumors or autoimmune disease
                                                                                                                                                                    264pp; English
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د
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Pred. No. 2.4e-80;
5; Mismatches 21;
                                                                                                                                                                                                                                                                                           Wonderling
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                                                                                                                                                                                                                                                                                           RS;
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RESULT 12
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   Matches 158;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   vaccines for therapeutic or prophylactic regulation of an immune response in animals (particularly cats, dogs, horses and humans). They may be used to treat autoimmune or infectious diseases including allergies, tumours, inflammation and graft rejection, and to increase the response from a co-administered antigen. The nucleotide sequences can also be used for the recombinant production of a protein, while nucleotide fragments are useful as probes, as amplification primers an as sources of inhibitory therapeutics (e.g., antisense oligonucleotides). The proteins may be used to raise antibodies and to screen for modulators of activity, while the antibodies may be used in detection, and in drug targetting.
                                                                                                                              16-JUL-1993;
13-AUG-1993;
24-AUG-1993;
19-NOV-1993;
03-DEC-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                   AAR66175 standard;
                                                                                                                                                                                                                                                                                                                       Flt3 ligand;
                                                                                                                                                                                                                                                                                                                                                                     10-AUG-1995
                                                                                              (INRM
                                                                                                                                                                                         19-MAY-1993;
07-JUL-1993;
                                                                                                                                                                                                                           18-MAY-1994;
                                                                                                                                                                                                                                                   24-NOV-1994.
                                                                                                                                                                                                                                                                           WO9426891-A
                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                               Human S86/S109 Flt3 ligand peptide sequence.
nucleic acid, vectors,
             New ligand for the Flt3
                                  WPI; 1995-006787/01
N-PSDB; AAQ79642.
                                                                        Birnbaum
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VAVNIQDEKHCKALWSLFLAQRWIEQLKTVAGSKMQTLLEDVNTEIHFVTSCTFQPLPEC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LRFVQTNISHLLQDTSQQLAALKPWITR--RNFSGCLELQCQPDSSTLVPPRSPGALEAT
                                                                                              INST NAT
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                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                       tyrosine kinase receptor ligand
                                                                      Culpepper
                                                                                                                               93US-0065231.
93US-0089263.
93US-0092549.
93US-0106340.
93US-0112391.
93US-0155111.
93US-0162413.
                                                                                                                                                                                                                              94WO-US05150
                                                                                              SANTE &
                                                                                                                                                                                                                                                                                                                                                                                                                      Peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              63.3%;
  host
                                                                        JA,
  tyrosine kinase receptor - host cells and antibodies, u
                                                                                                            RECH MEDICALE
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                                                                                                                                                                                                                                                                                                                                                                                                                      235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 774; DB 21;
Pred. No. 1.3e-69;
3; Mismatches 38;
                                                                        Hannum CH,
                                                                                                                                                                                                                                                                                                                                                                                                                      AA
                                                                          Lee
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 294;
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    and related
useful for

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RESULT 13
AAB20194
ID AAB20194
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A cDNA library from the human stromal cell line 29SV48, in pME18S, was screened with an 800 bp fragment derived from mouse clone T118. This fragment encompasses the coding region conserved between two mouse clones, T118 and T110. Approx. 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 11; Page 76-77; 90pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      treating abnormal cell physiology and proliferation, e.g. cancer, also for diagnosis and drug screening % \left( 1\right) =\left\{ 1\right\} =\left\{
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           rlt-3 ligand; Fms-like tyrosine kinase; human; vaccine;
immunotherapy; therapy; tumour; cancer; melanoma; gliom
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                        Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        lymphoma;
                                                                                                                  WO200109303-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           \tt VASNLQDEELCGALWRLVLAQRWMERLKTVAGSKMQGLLERVNTEIHFVTKCAFQPPPSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VAVNLQDEKHCKALWSLFLAQRWIEQLKTVAGSKMQTLLEDVNTEIHFVTSCTFQPLPEC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LRFVQTNISRLLQETSEQLVALKPWITR-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Flt-3 ligand
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              therapy; tumour; cancer; melanoma; glic
immune disease; infection; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                     /label=
27..182
/label=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /label=
27...235
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                                                                                                                                                                                                                                                                                                                               /label= Transmembrane_domain
                                                                                                                                                                                                                        /label= Cytoplasmic_domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Extracellular_domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mature_protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Signal_peptide
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Pred. No. 1.4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AΑ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            42;
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RESULT 14
AAR67541
ID AAR67
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ligand-encoding polynucleotide, and 1 or more antiger or cytokine-encoding polynucleotides. The Fit-3 ligand-encoding polynucleotides. The Fit-3 ligand-encoding polynucleotides are incorporated into polynucleotide may encode the present full-length human Fit-3 confidence of the Fit-3 ligand. The polynucleotides are incorporated into the cells of the vertebrate in vivo, and a prophylactically or therapeutically effective amount of Fit-3 ligand and 1 or more antigens or cytokines is produced in vivo. Pharmaceutical compositions comprising the polynucleotides are useful for suppressing tumour growth in a mammal. The tumour is melanoma, galioma or lymphoma, particularly B-cell lymphoma. They can also be used for the prophylactic and/or therapeutic treatment of:

(a) bacterial (e.g. Bacillus infections), vital (e.g. hepatitis B and C in humans), parasitic (e.g. malaria) and fungal infections;
                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local S
Matches 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present sequence is that of human Fms-like tyrosine kinase (Flt-3 ligand). The invention is directed to enhancing the immune response of a vertebrate to an antigen or a cytokine by administering in vivo, into a tissue of a vertebrate, a Flt-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (b) autoimmune diseases (e.g. rheumatoid arthritis and
osteoarthritis); (c) cancer; and (d) Aujeszky's disease in pigs
Various other examples of these diseases are given in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 2; Page 137-138; 149pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Immunogenic compositions comprising Fit-3 ligand encoding polynuclectide and one or more antigen, or cytokine encoding polynuclectides, useful for suppressing tumour growth and for treating autoimmune diseases (e.g. rheumatoid arthritis) -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB;
                05-AUG-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               specification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hermanson
                                            AAR67541;
                                                                        AAR67541 standard; Protein; 235
                                                                                                                                                 178
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                                                                                                                                                                                                                                                                                                                          ELPEPRPRQLLLLLLLPLTLVLLAAAWGLRWQRARRR----GELHPGVPLP 228
                                                                                                                                              LREVQTNISHLLKDTCTQLLALKPCIGKACQNESRCLEVQCQPDSSTLLPPRSPIALEAT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2001-123319/13.
DB; AAF30312.
                                                                                                                                                                                                                                                                  VASNLQDEELCGALWRLVLAQRWMERLKTVAGSKMQGLLERVNTEIHEVTKCAFQPPPSC
                                                                                                                                                                                                                                                                                               VAVNLQDEKHCKALWSLFLAQRWIEQLKTVAGSKMQTLLEDVNTEIHFVTSCTFQPLPEC 120
                                                                                                                                                                                                          LRFVQTNISRLLQETSEQLVALKPWITR - - QNFSRCLELQCQPDSSTLPPPWSPRPLEAT
                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                  235 AA;
                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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              (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                     Score 772.5; DB 22; Pred. No. 1.4e-69;
                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human flt-3 ligand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Peptide
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25-AUG-1993;
03-DEC-1993;
07-MAR-1994;
11-MAY-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                         A human T-cell lambda-gt10 random primed cDNA library was screened with a fragment corresponding to the extracellular domain of mouse fit3 ligand (flt3-L) (nt 103-516 of AAQ79076) to isolate human flt3-L cDNA. Flt-3 stimulates progenitor and stem cells, and can be used e.g. in gene therapy protocols.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Page 29-30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Isolated ligands for flt 3 receptors - anaemia, AIDS and various cancers {\bf r}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Flt-3 ligand; flt3-L; anemia; cancer; AIDS; gene therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Beckmann MP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24-MAY-1993;
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                     181 ELPEPRPRQLLLLLLLLPLTLVLLAAAWGLRWQRARRR-----GELHPGVPLP 228
                                                                                                                   121 LRFVQTNISHLLKDTCTQLLALKPCIGKACQNFSRCLEVQCQPDSSTLLPPRSPIALEAT 180
                                                                                                                                                                                                                                                                   1 MTVLAPAWSPNSSLLLLLLLLLSPCLRGTPDCYFSHSPISSNFKVKFRELTDHLLKDYPVT
                                                                                                                                                                                  VAVNLQDEKHCKALWSLFLAQRWIEQLKTVAGSKMQTLLEDVNTEIHFVTSCTFQPLPEC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1995-008071/02
                                                                                                                                                                                                                                         MTVLAPAWSP-TTYLLLLLLSSGLSGTQDCSFQHSPISSDFAVKIRELSDYLLQDYPVT
APTAPOPP---LLLLLLPVGLLLLAAAWCLHWQRTRRRTPRPGEQVPPVPSP
                                                                        LREVQTNISRLLQETSEQLVALKPWITR-
                                                                                                                                                             VASNLQDEELCGGLWRLVLAQRWMERLKTVAGSKMQGLLERVNTEIHFVTKCAFQPPPSC
                                                                                                                                                                                                                                                                                                                          al Similarity
163; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAQ79079
                                                                                                                                                                                                                                                                                                                                                                                                      235 AA;
                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lyman
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93US-0162407.
94US-0209502.
94US-0243545.
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93US-0106463
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206..235
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                         62.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      33pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cytoplasmic_domain
                                                                                                                                                                                                                                                                                                                     Score 768.5; DB 1
Pred. No. 3.6e-69;
7; Mismatches 43
                                                                            QNFSRCLELQCQPDSSTLPPPWSPRPLEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   useful
                                                                                                                                                                                                                                                                                                                                                               DB 16;
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                                                                                                                                                                                                                                                                                                                        43;
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                                                                                                                                                                                                                                                                                                                                                               Length
                                                                                                                                                                                                                                                                                                                                                                 . 235;
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RESULT 15
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                                                                                                                                                                                                                                                                                              A method has been developed of initiating or enhancing: (i) an antigen-
CC specific immune tolerance; or (ii) immunotolerance of a therapeutic
CC immunogenic molecule by addition of a polypeptide, before, after or with
CC the mucosal administration of an immunotolerising amount of the antigen
CC threapeutic molecule, respectively. The polypeptide is capable of
CC binding the flt3 receptor and is: a) amino acids 28-x of murine flt3
CC ligand (flt3-L), where x is an amino acid between 163-231; b) amino
CC acids 28-y of human flt3-L, where y is an amino acid between 160-235;
CC and c) a polypeptide that has at least 90% identity to the polypeptides
CC diseases, food allergies or organ or tissue rejection following
CC transplantation. Administration of flt3-L allows lower doses of antigens
CC to be used in vivo for mucosally administered antigens. The present
                       δÃ
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Best Local Similarity
Matches 163; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAW67769 standard; Protein; 235 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Antigen-specific peripheral immune tolerance; flt3-ligand; flt3-L; immunogenic; autoimmune disease; organ transplantation; food allergy; tissue transplantation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAW67769;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Methods for initiating or enhancing antigen specific immune tolerance - by using murine or human flt3 ligand
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; Page 14-15; 25pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1999-070422/06.
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                                                                                                                                                                                                                                                                          Sequence
178 APTAPQPP--LLLLLLLPVGLLLLAAAWCLHWQRTRRRTPRPGEQVPPVPSP 227
                                                     181 ELPEPRPROLLLLLLLPLTLYLLAAAWGLRWQRARRR----GELHPGVPLP 228
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Search completed: November 24, 2002, 10:10:13 Job time : 32.2296 secs

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Result
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      US-09-448-378-1
US-09-983-806-6
US-09-904-536-1
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US-09-904-536-14
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US-09-904-536-18
US-09-904-536-18
US-09-904-536-17
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US-09-983-806-2
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Sequence 17, Appl
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US-09-793-139-4	US-09-867-550-2026	US-10-052-586-414	US-09-989-721-57	US-09-990-456-57	US-09-993-604-57	US-09-991-163-57	US-09-990-442-57	US-09-991-073-57	US-09-989-732-57	US-09-989-731-57	US-09-989-727-57	US-09-989-279-57	US-09-989-723-57	US-09-989-722-57	US-09-187-368-1	US-09-992-598-57	US-09-987-107-35	US-09-800-729-208	US-09-211-755B-47	US-09-818-879-47	US-09-793-139-47	US-09-826-508-26	US-09-867-852-2	US-09-948-018-2	US-09-867-852-142
Sequence 4, Appli	Sequence 2026, Ap	Sequence 414, App	Sequence 57, Appl	Sequence 57, Appl	Sequence 57, Appl	57,	Sequence 57, Appl	Sequence 57, Appl	57,	Sequence 57, Appl	Sequence 1, Appli		Sequence 35, Appl	Sequence 208, App	47,	Sequence 47, Appl	47,	Sequence 26, Appl	Sequence 2, Appli	Sequence 2, Appli	Sequence 142, App				

## ALIGNMENTS

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US-10-095-449-2
Sequence 2, Application US/10095449
Patent No. US20020160004A1
GENERAL INFORMATION:
REFERENCE/DOCKET NUMBER: 2813-C TELECOMMUNICATION INFORMATION: TELEPHONE: (206) 587-0430
                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/10/095,449
FILING DATE: 13-Mar-2002
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 7.0.1
SOFTWARE: Microsoft Word, Version #5.1
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                      ATTORNEY/AGENT INFORMATION:
NAME: Malaska, Stephen L.
REGISTRATION NUMBER: 32,6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Lyman, Stewart D.
Beckmann, M. Patricia
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TITLE OF INVENTION: Ligands for flt3/flk-2 Receptors
                                                                                                                                        APPLICATION NUMBER: US/08/162,407
FILLING DATE: December 3, 1993
APPLICATION NUMBER: 08/111,758
FILLING DATE: August 25, 1993
APPLICATION NUMBER: 08/106,463
FILLING DATE: August 12, 1993
APPLICATION NUMBER: 08/068,394
FILLING DATE: May 24, 1993
                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: 08/669,692 FILING DATE: 24-JUN-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: US
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STREET: 51 University Street
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TELEFAX: (206) 233-0644

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                           RESULT
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; SEQ ID NO 2
; LENGTH: 231
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Best Local Similarity
Matches 231; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Brasel, Kenneth
TITLE OF INVENTION: Dendr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILE REFERENCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
                                                                          181 ELPEPRPRQLLLLLLLLPLTLVLLAAAWGLRWQRARRRGELHPGVPLPSHP 231
                                                                                           181 ELPEPRPRQLLLLLLLLPLTLVLLAAAWGLRWQRARRRGELHPGVPLPSHP 231
                                                                                                                                             121
                                                                                                                                                           121 LRFVQTNISHLLKDTCTQLLALKPCIGKACQNFSRCLEVQCQPDSSTLLPPRSPIALEAT 180
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                                                                                                                                                                                                             61
                                                                                                                                                                                                                           61 VAVNLQDEKHCKALWSLFLAQRWIEQLKTVAGSKMQTLLEDVNTEIHFVTSCTFQPLPEC 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Match 100.0%;
Local Similarity 100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                          LRFVQTNISHLLKDTCTQLLALKPCIGKACQNFSRCLEVQCQPDSSTLLPPRSPIALEAT
                                                                                                                                                                                                          VAVNLQDEKHCKALWSLFLAQRWIEQLKTVAGSKMQTLLEDVNTEIHFVTSCTFQPLPEC
                                                                                                                                                                                                                                                                           MTVLAPAWSPNSSLLLLLLLSPCLRGTPDCYFSHSPISSNFKVKFRELTDHLLKDYPVT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MTVLAPAWSPNSSLLLLLLLLSPCLRGTPDCYFSHSPISSNFKVKFRELTDHLLKDYPVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PatentIn version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 231 amino acids
                                                                                                                                                                                                                                                                                                                                         100.0%; Score 1223; DB 10; ilarity 100.0%; Pred. No. 1.5e-107; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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; SEQUENCE DESCRIPTION: SEQ ID NO: US-09-983-806-2
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                                                                                                                                                                                                                                                                                                                                              Matches
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEX: 756822
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
181
                                        181 ELPEPRPRQLILLLLLLPLTLVLLAAAWGLRWQRARRRGELHPGVPLPSHP 231
                                                                                    121
                                                                                                      121 LRFVQTNISHLLKDTCTQLLALKPCIGKACQNFSRCLEVQCQPDSSTLLPPRSPIALEAT
                                                                                                                                                                                             61 VAVNLQDEKHCKALWSLFLAQRWIEQLKTVAGSKMQTLLEDVNTEIHFVTSCTFQPLPEC
                                                                                                                                                                    61 VAVNLQDEKHCKALWSLFLAQRWIEQLKTVAGSKMQTLLEDVNTEIHFVTSCTFQPLPEC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: 2813-C TELECOMMUNICATION INFORMATION: TELEPHONE: (206) 587-0430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
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TITLE OF INVENTION: Ligands for flt3/flk-2 Receptors
NUMBER OF SEQUENCES: 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA
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Beckmann, M. Patricia
ELPEPRPRQLILLILLIPLTLVLLAAAWGLRWQRARRRGELHPGVPLPSHP
                                                                                {\tt LRFVQTNISHLLKDTCTQLLALKPCIGKACQNFSRCLEVQCQPDSSTLLPPRSPIALEAT}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US 08/162,407 FILING DATE: 03-DEC-1993 APPLICATION NUMBER: 08/111,758 FILING DATE: August 25, 1993 APPLICATION NUMBER: 08/106,463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: August 12, 1993
APPLICATION NUMBER: 08/068,394
FILING DATE: May 24, 1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/09/983,806 FILING DATE: 25-Oct-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: Apple Macintosh 7 OPERATING SYSTEM: Macintosh 7 SOFTWARE: Microsoft Word, Ver:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 231 amino acids TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REGISTRATION NUMBER: 32,655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/08/444,626 FILING DATE: 19-MAY-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Stephen L. Malaska, STREET: 51 University Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                         100.0%; Score 1223; DB 10; ilarity 100.0%; Pred. No. 1.5e-107; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              233-0644
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231
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RESULT 4

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US-10-095-449-6
; Sequence 6, Application US/10095449
; Patent No. US20020160004A1
; GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
121
                                                                                                                                                     60 VASNLQDEELCGGLWRLVLAQRWMERLKTVAGSKMQGLLERVNTEIHFVTKCAFQPPPSC 119
                                                                                                                                                                           61 VAVNLQDEKHCKALWSLFLAQRWIEQLKTVAGSKMQTLLEDVNTEIHFVTSCTFQPLPEC 120
                                                                                                                                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                                   1 MTVLAPAWSPNSSLLLLLLLSPCLRGTPDCYFSHSPISSNFKVKFRELTDHLLKDYPVT 60
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MEDIUM TYPE: Floppy disk
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Beckmann, M. Patricia
TITLE OF INVENTION: Ligands for flt3/flk-2 Receptors
                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear MOLECULE TYPE: protein SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
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                                                                           LRFVQTNISRLLQETSEQLVALKPWITR--QNFSRCLELQCQPDSSTLPPPWSPRPLEAT 177
                                                                                                                                                                                                                               LRFVQTNISHLLKDTCTQLLALKPCIGKACQNFSRCLEVQCQPDSSTLLPPRSPIALEAT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/08/162,407
FILING DATE: December 3, 1993
APPLICATION NUMBER: 08/111,758
FILING DATE: August 25, 1993
APPLICATION NUMBER: 08/106,463
FILING DATE: August 12, 1993
APPLICATION NUMBER: 08/06,394
FILING DATE: May 24, 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REGISTRATION NUMBER: 32,655
REFERENCE/DOCKET NUMBER: 2813-C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Malaska, Stephen L. REGISTRATION NUMBER: 32,6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 13-Mar-2002 CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/10/095,449
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OPERATING SYSTEM: Macintosh 7.0.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (206) 233-0644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 24-JUN-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 235 amino acids
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                                                                                                                                                                                                                                                                                                                            62.8%;
70.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (206) 587-0430
                                                                                                                                                                                                                                                                                                     17; Mismatches
                                                                                                                                                                                                                                                                                                                           Score 768.5; DB 9
Pred. No. 6.5e-65;
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                                                                                                                                                                                                                                                                                                         Gaps
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; LENGTH: 235
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-448-378-1
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US-09-448-378-1
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US-09-983-806-6
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SEQ ID NO 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 6, Application US/09983806 Patent No. US20020107365A1 GENERAL INFORMATION:
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Best Local Similarity
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CURRENT FILING DATE: 1999-11-23
NUMBER OF SEQ ID NOS: 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 LRFYQTNISHLLKDTCTQLLALKPCIGKACQNFSRCLEVQCQPDSSTLLPPRSPIALEAT 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MTVLAPAWSP-TTYLLLLLLLSSGLSGTQDCSFQHSPISSDFAVKIRELSDYLLQDYPVT
                                                                                                                                                                  CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/983,806
FILING DATE: 25-Oct-2001
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Beckmann, M. Patricia
TITLE OF INVENTION: Ligands for flt3/flk-2 Receptors
NUMBER OF SEQUENCES: 8
                                                                                                                                                  PRIOR APPLICATION DATA
                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Lyman, Stewart D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VASNLQDEELCGGLWRLVLAQRWMERLKTVAGSKMQGLLERVNTEIHFVTKCAFQPPPSC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       163;
                                                                                                                                                                                                                                            COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 7.0.1
SOFTWARE: Microsoft Word, Version
                                                                                                                                                                                                                                                                                                                                                                                CITY: Seattle
STATE: Washington
APPLICATION NUMBER: 08/111,758 FILING DATE: August 25, 1993 APPLICATION NUMBER: 08/106,463 FILING DATE: August 12, 1993
                                                    APPLICATION NUMBER: US 0 FILING DATE: 03-DEC-1993 APPLICATION NUMBER: 08/1
                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Stephen L. Malaski
STREET: 51 University Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Brasel, Kenneth
                                                                                                            APPLICATION NUMBER: US/08/444,626 FILING DATE: 19-MAY-1995
                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PatentIn version 3.0
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Pred. No. 6.5e-65;
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                                                                                            08/162,407
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                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS: 20
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1
LENGTH: 235
TYPE: PRT
                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:

APPLICANT: Graddis, Thomas J.

APPLICANT: McGrew, Jeffrey T.

APPLICANT: MCGrew, Jeffrey T.

TITLE OF INVENTION: ELT3-L MUTANTS AND METHODS OF USE
FILE REFERENCE: 03260.0028

CURRENT FILING DATE: 2001-07-16

PRIOR APPLICATION NUMBER: PRIOR APPLICATION: 09/109,100

PRIOR FILING DATE: 1999-07-02
                                                                                                                                        Matches
                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1, Application US/09904536 Patent No. US20020111475A1
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INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       178 APTAPQPP--LLLLLLLPVGLLLLAAAWCLHWQRTRRRTPRPGEQVPPVPSP 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   181 ELPEPRPRQLLLLLLLEPLTLVLLAAAWGLRWQRARRR----GELHPGVPLP 228
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hes 163;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Malaska, Stephen L.
REGISTRATION NUMBER: 32,655
REFERENCE/DOCKET NUMBER: 2813-C
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
TELEFAX: (206) 233-0644
                                                                                   MTVLAPAWSPNSSLLLLLLLLSPCLRGTPDCYFSHSPISSNFKVKFRELTDHLLKDYPVT 60
VAVNLQDEKHCKALWSLFLAQRWIEQLKTVAGSKMQTLLEDVNTEIHFVTSCTFQPLPEC 120
                                                                MTVLAPAWSPNSSLLLLLLLSPCLRGTPDCYFSHSPISSNFKVKFRELTDHLLKDYPVT 60
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                                                                                                                                          163;
                                                                                                                                                      Similarity
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                                                                                                                                        Conservative
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                                                                                                                                                     62.8%; Score 768.5; DB 170.3%; Pred. No. 6.5e-65;
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Pred. No. 6.5e-65;
                                                                                                                                     Mismatches
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; ORGANISM: Homo sapiens US-09-904-536-10
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                                                                                                                            SEQ ID NO 10
LENGTH: 212
                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Graddis, Thomas J.
APPLICANT: McGrew, Jeffrey T.
APPLICANT: MCGrew, Jeffrey T.
TITLE OF INVENTION: FLT3-L MUTANTS AND METHODS OF USE
FILE REFERENCE: 03260.0028
     Matches 144;
                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                              Sequence 10, Application US/09904536 Patent No. US20020111475A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 136; Conserv
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                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/09/904,536 CURRENT FILING DATE: 2001-07-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Graddis, Thomas J.
APPLICANT: McGrew, Jeffrey T.
TITLE OF INVENTION: FLT3-L MUTANTS AND METHODS
FILE REFERENCE: 03260,0028
CURRENT APPLICATION NUMBER: US/09/904,536
CURRENT FILING DATE: 2001-07-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 19, Application US/09904536 Patent No. US20020111475A1
                                                                                                                                                             NUMBER OF SEQ ID NOS: 20
SOFTWARE: Patentt
                                                                                                                                                                                                PRIOR APPLICATION NUMBER: PRIOR APPLICATION: 09/109,100 PRIOR FILING DATE: 1999-07-02
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                                                                                                             TYPE: PRT
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TYPE: PRT
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   Conservative
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                    56.6%;
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99.3%;
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 Score 692; DB
Pred. No. 8.5e
15; Mismatches
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Pred. No. 4.
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 DB 10;
3.5e-58;
nes 39;
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                                 Length 212;
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PRIOR EILING DATE: 1999-07-02
NUMBER OF SEQ ID NOS: 20
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 15
                                                                                                                                                                                                        Sequence 14, Application US/09904536 Patent No. US20020111475A1
                                                                                                                                                                                     GENERAL INFORMATION:
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         APPLICANT: Graddis, Thomas J.
APPLICANT: McGrew, Jeffrey T.
TITLE OF INVENTION: FLI3-L MUTANTS AND METHODS OF USE
FILE REFERENCE: 03260.0028
CURRENT APPLICATION NUMBER: US/09/904,536
CURRENT FILING DATE: 2001-07-16
PRIOR APPLICATION NUMBER: PRIOR APPLICATION: 09/109,100
PRIOR FILING DATE: 1999-07-02
NUMBER OF SEQ ID NOS: 20
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APPLICANT: McGrew, Jeffrey T.
TITLE OF INVENTION: FLT3-L MUTANTS AND METHODS
FILE REFERENCE: 03260,0028
CURRENT APPLICATION NUMBER: US/09/904,536
CURRENT FILING DATE: 2001-07-16
SOFTWARE: PatentIn Ver.
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TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                              WGLRWQRARRR----GELHPGVPLP 228
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Pred. No. 2.4e-57;
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RESULT 13
US-09-904-536-16
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-904-536-14
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LENGTH: 209
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Best Local :
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APPLICANT: McGrew, Jeffrey T.
TITLE OF INVENTION: FLT3-L MUTANTS AND METHODS OF USE
FILE REFERENCE: 03260.0028
CURRENT APPLICATION NUMBER: U$709/904,536
CURRENT FILING DATE: 2001-07-16
PRIOR APPLICATION NUMBER: PRIOR APPLICATION: 09/109,100
PRIOR FILING DATE: 1999-07-02
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Pred. No. 3e-57;
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Sequence 16, Application US/09904536 Patent No. US20020111475A1

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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-904-536-9
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-904-536-16
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PRIOR FILING DATE: 1999-07-02
NUMBER OF SEQ ID NOS: 20
SOFTMARE: Patentin Ver. 2.1
SEQ ID NO 15
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APPLICANT: Graddis, Thomas J.
APPLICANT: McGrew, Jeffrey T.
TITLE OF INVENTION: FLT3-L MUTANTS AND METHODS OF USE
FILE REFERENCE: 03260.0028
                                                                                                                                                                                                         Best Local Similarity Matches 142; Conserv
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Best Local Similarity
Matches 143; Conserv
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APPLICANT: McGrew, Jeffrey T.
TITLE OF INVENTION: FLT3-L MUTANTS AND METHODS
FILE REFERENCE: 03260.0028
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CURRENT FILING DATE: 2001-07-16
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CURRENT FILING DATE: 2001-07-16
177
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Pred. No. 7.2e-57;
5; Mismatches 40;
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Pred. No. 3.8e-57;
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                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity Matches 142; Conserv
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SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Graddis, Thomas J.
APPLICANT: McGrew, Jeffrey T.
TITLE OF INVENTION: FLT3-L MUTANTS AND METHODS
FILE REFERENCE: 03260.0028
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/904,536
CURRENT FILING DATE: 2001-07-16
PRIOR APPLICATION NUMBER: PRIOR APPLICATION: 09/109,100
PRIOR FILING DATE: 1999-07-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 209
TYPE: PRT
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                                                                                                       208 WGLRWQRARRR----GELHPGVPLP 228
                                                                                                                                           121 R--QNFSRCLELQCQPDSSTLPPPWSPRPLEATAPTAPQPP--LLLLLLLPVGLLLLAAA 176
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                                                                      WCLHWQRTRRRTPRPGEQVPPVPSP
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                                                                                                                                                                                                               KTVAGSKMQGLLERVNTEIHFVTKCAFQPPPSCLRFVQTNISRLLQETSEQLVALKPWIT 120
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Pred. No. 7.2e-57;
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Match
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PCT-US98-12085-2
US-08-068-394-2
US-08-106-463-2
US-08-111-758-2
US-08-111-758-2
US-08-162-407-2
US-08-444-625-2
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Sequence 23, Appl	34, 2	34,	34,	34,	34,	34,	7	7,	7,	7	H	15,	11, App	1857	e 17,	20,	9	18, 1	25,	equence 25,	516	1	e 8678	38,	•	38,	38,	38,	38,	,2	2,	equence 2,	equence 8,	'n	equence 2,	ce 2,	, P	e 2, Appl

# ALIGNMENTS

RESULT 1 PCT-US98-12085-2

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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM/PC Compatible
COMPUTER: IBM/PC Compatible
COMPUTER: IBM/PC Compatible
OPERATING SYSTEM: MS-DOS/Windows 95
SOFTWARE: Word for Windows 95, Version 7.(
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US98/12085
FILING DATE: 12-JUN-1998
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 32,655
PRICED TO TO TO THE TO T
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TITLE OF INVENTION: A Method of Enhancing Antigen-Specific Peripheral Immune NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                          REFERENCE/DOCKET NUMBER: 28 TELECOMMUNICATION INFORMATION:
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TELEPHONE:
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(206) 587-0430
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TELEX: 756822
INFORMATION FOR SEQ ID NO:

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TELEFAX: 12.

(206) 233-0644

SEQUENCE CHARACTERISTICS

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RESULT 2
US-08-068-394-2
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                         Query Match
Best Local Similarity
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Best Local Similarity
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INFORMATION FOR SEQ ID NO:
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                                             3-068-394-2
                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPAILIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                 MOLECULE TYPE:
                                                                                                                     SEQUENCE CHARACTERISTICS
                                                                                                                                                                 TELECOMMUNICATION INFORMATION: TELEPHONE: (206) 587-0430 TELEFAX: (206) 233-0644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Lyman, Stewart D.
APPLICANT: Beckmann, M. Patricia
TITLE OF INVENTION: Ligands for flt3/flk-2 Receptors
NUMBER OF SEQUENCES: 4
                                                                                                                                                                                                                                                 CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
                                                                                             LENGTH:
                                                                                 TOPOLOGY:
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CITY: Seattle
                                                                                                                                                                                                                         REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                          STATE:
                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY:
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       Score 1223; DB 4;
Pred. No. 3.5e-110;
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Pred. No. 3.5e-110;
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                                                                                                                                                                                  Matches 231;
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                                                                                                                                                                                                                                                                                                                                              TELEX: 756822
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                            TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 231 amino acids
                                                                                                                                                                                                                                                                                                                                                                                           REGISTRATION NUMBER: 32,655
REFERENCE/DOCKET NUMBER: 28
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
APPLICATION NUMBER: US,
FILING DATE: 19930812
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Lyman, Stewart D.
APPLICANT: Beckmann, M. Patricia
TITLE OF INVENTION: Ligands for flt3/flk-2 Receptors
NUMBER OF SEQUENCES: 6
                    121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (L. 756822
                                                    61
                                                              61 VAVNLQDEKHCKALWSLFLAQRWIEQLKTVAGSKMQTLLEDVNTEIHFVTSCTFQPLPEC 120
                                                                                                                                                                                                   Local
                                                                                                                                                                                                                                                                                                  TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          181
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                                                                                                                               1 MTVLAPAWSPNSSLLLLLLLLSPCLRGTPDCYFSHSPISSNFKVKFRELTDHLLKDYPVT 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Seattle
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                                               VAVNLQDEKHCKALWSLFLAQRWIEQLKTVAGSKMQTLLEDVNTEIHFVTSCTFQPLPEC 120
                                                                                                              {\tt MTVLAPAWSPNSSLLLLLLLLSPCLRGTPDCYFSHSPISSNFKVKFRELTDHLLKDYPVT}
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                                                                                                                                                                                                 Similarity
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                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Stephen L.
                                                                                                                                                                                        100.0%; Score 1223; DB 5; 100.0%; Pred. No. 3.5e-110;
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GENERAL INFORMATION:
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Lyman, Stewart D.
APPLICANT: Beckmann, M. Patricia
TITLE OF INVENTION: Ligands for flt3/flk-2 Receptors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REGISTRATION NUMBER: 32,655
REFERENCE/DOCKET NUMBER: 28.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
TELEPAX: (206) 233-0644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 7.0.1
SOFTWARE: Microsoft Word, Version #5.
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: 08/106,463 FILING DATE: August 12, 1993 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: 08/06 FILING DATE: May 24, 1993 ATTORNEY/AGENT INFORMATION: NAME: Malaska, Stephen L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS: LENGTH: 231 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES:
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TELEFAX: 756822
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CITY: S
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                181 ELPEPRPRQLLLLLLLLLPLTLVLLAAAWGLRWQRARRRGELHPGVPLPSHP 231
                                                                                                 121 LRFVQTNISHLLKDTCTQLLALKPCIGKACQNFSRCLEVQCQPDSSTLLPPRSPIALEAT 180
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                                                                                                                                                      61 VAVNLQDEKHCKALWSLFLAQRWIEQLKTVAGSKMQTLLEDVNTEIHFVTSCTFQPLPEC
                                                                                                                                                                         61 VAVNLQDEKHCKALWSLFLAQRWIEQLKTVAGSKMQTLLEDVNTEIHFVTSCTFQPLPEC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER:
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                                                                                                                                                                                                                                                    1 MTVLAPAWSPNSSLLLLLLLLSPCLRGTPDCYFSHSPISSNFKVKFRELTDHLLKDYPVT 60
                                                                                                                                                                                                                                  1 MTVLAPAWSPNSSLLLLLLLLSPCLRGTPDCYFSHSPISSNFKVKFRELTDHLLKDYPVT 60
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                                                                           LRFYQTNISHLLKDTCTQLLALKPCIGKACQNFSRCLEVQCQPDSSTLLPPRSPIALEAT
ELPEPRPROLLLLLLLLPLTLVLLAAAWGLRWQRARRRGELHPGVPLPSHP
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                                                                                                                                                                                                                                                                                                             100.0%; Score 1223; DB 5; nilarity 100.0%; Pred. No. 3.5e-110; Conservative 0; Mismatches 0;
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DN: 435
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RESULT 5
US-08-162-407-2
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GENERAL INFORMATION:
APPLICANT: Lyman, Stewart D.
APPLICANT: Beckmann, M. Patricia
                                                                                                                                                                                                                                                                 Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 231; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: MICROSOFT WORD, Version #5
CURRENT APPLICATION NUMBER: US/08/162,407
FILING DATE: December 3, 1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/111,758
FILING DATE: August 25, 1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/106,463
FILING DATE: August 12, 1993
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 08/068,394
FILING DATE: May 24, 1993
ATTORNEY/AGENT INFORMATION:
NAME: Malasks Stanker.
                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: Ligands for flt3/flk-2 Receptors NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 231 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION: TELEPHONE: (206) 587-0430
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OPERATING SYSTEM: Macintosh
181
               181 ELPEPRPRQLLLLLLLLLPLTLYLLAAAWGLRWQRARRRGELHPGVPLPSHP
                                                                COUNTRY:
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                                                                                                                                                               61 VAVNLQDEKHCKALWSLFLAQRWIEQLKTVAGSKMQTLLEDVNTEIHFVTSCTFQPLPEC
                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REGISTRATION NUMBER: 32,655
REFERENCE/DOCKET NUMBER: 2813-C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Malaska, Stephen L. REGISTRATION NUMBER: 32,6
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RESULT 6 US-08-444-625-2

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: August 12, 1993
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/068,394
FILING DATE: May 24, 1993
CLASSIFICATION: 424
ATTORNEY JACES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2, Application US/08444625 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO:
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OPERATING SYSTEM: Macintosh 7.0.1
SOFTWARE: Microsoft Word, Version #5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/444,625
FILING DATE: 19-MAY-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: 28: TELECOMMUNICATION INFORMATION: TELEPHONE: (206) 587-0430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 03-DEC-1993
APPLICATION NUMBER: 08/111,758
FILING DATE: August 25, 1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/106,463
                                                   SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: Malaska, Stephen L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 03-DEC-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
                                                                                                                                     121 LREVQTNISHLLKDTCTQLLALKPCIGKACQNFSRCLEVQCQPDSSTLLDPRSPIALEAT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (200.
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CORRESPONDENCE ADDRESS:
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APPLICANT: Beckmann, M. Patricia
TITLE OF INVENTION: Ligands for flt3/flk-2 Receptors
                                                                                                                            121
                                                                                                                                                                                     61 VAVNLQDEKHCKALWSLFLAQRWIEQLKTVAGSKMQTLLEDVNTEIHFVTSCTFQPLPEC
                                                                                                                                                                                                      61 VAVNLQDEKHCKALWSLFLAQRWIEQLKTVAGSKMQTLLEDVNTEIHFVTSCTFQPLPEC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REGISTRATION NUMBER: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (206) 233-0644
                                                                                                                                                                                                                                                                                                                                                                                                                          linear
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; Sequence 2, Application US/08444626
; GENERAL INFORMATION:
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Best Local Similarity
                                                                                                                                                                                                                                                         Matches 231;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         REGISTRATION NUMBER: 32,655
REFERENCE/DOCKET NUMBER: 32
TELECOMMUNICATION INFORMATION
TELEPHONE: (206) 587-0430
                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 231 amino acids
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 03-DEC-1993
APPLICATION NUMBER: 08/711,758
FILING DATE: August 25, 1993
PRIOR APPLICATION DATA: 08/106,463
APPLICATION NUMBER: 08/106,463
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CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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APPLICANT: Beckmann, M. Patricia
TITLE OF INVENTION: Ligands for flt3/flk-2 Receptors
NUMBER OF SEQUENCES: 8
                                     181
                                                                  121
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                                                                                                                                            61 VAVNLQDEKHCKALWSLFLAQRWIEQLKTVAGSKMQTLLEDVNTEIHFVTSCTFQPLPEC 120
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                                                                                                                                                                                    NAME: Malaska, Stephen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
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ELPEPRPRQLLLLLLLLTLVLLAAAWGLRWQRARRRGELHPGVPLPSHP 231
                   ELPEPRPRQLLLLLLLLPLTLVLLAAAWGLRWQRARRRGELHPGVPLPSHP 231
                                                                              LRFVQTNISHLLKDTCTQLLALKPCIGKACQNFSRCLEVQCQPDSSTLLPPRSPIALEAT 180
                                                            LRFVQTNISHLLKDTCTQLLALKPCIGKACQNFSRCLEVQCQPDSSTLLPPRSPIALEAT
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51 University Street
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Pred. No. 3.5e-110;
); Mismatches 0;
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US-08-444-632-2
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Вþ
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APPLICATION NUMBER: 08/111,758
FILING DATE: 08/211,758
FILING DATE: August 25, 1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/106,463
FILING DATE: August 12, 1993
FILING DATE: August 12, 1993
                                                                                                                                                                                                                                                                                          Matches
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PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 08/162,407
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MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 7.0.1
SOFTWARE: Microsoft Word, Version
CURRENT APPLICATION DATA:
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APPLICANT: Beckmann, M. Patricia
TITLE OF INVENTION: Ligands for flt3/flk-2 Receptors
NUMBER OF SEQUENCES: 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REGISTRATION NUMBER: 32,655
REFERENCE/DOCKET NUMBER: 2813-C
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION:
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                                                                                      121 LRFVQTNISHLLKDTCTQLLALKPCIGKACQNFSRCLEVQCQPDSSTLLPPRSPIALEAT 180
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181
                                  181 ELPEPRPRQLLLLLLLLPLTLVLLAAAWGLRWQRARRRGELHPGVPLPSHP 231
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                                                                                                                                                                                                                                                                                         Match 100.0%; Score 1223; DB 8; Local Similarity 100.0%; Pred. No. 3.5e-110; les 231; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE:
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                                                                                                                                                                                                                                   MTVLAPAWSPNSSLLLLLLLLSPCLRGTPDCYFSHSPISSNFKVKFRELTDHLLKDYPVT
                                                                                                                                            VAVNLQDEKHCKALWSLFLAQRWIEQLKTVAGSKMQTLLEDVNTEIHFVTSCTFQPLPEC
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LRFVQTNISHLLKDTCTQLLALKPCIGKACQNFSRCLEVQCQPDSSTLLPPRSPIALEAT
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US-08-669-692-2
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GENERAL INFORMATION:
APPLICANT: Lyman, Stewart D.
APPLICANT: Beckmann, M. Patricia
TITLE OF INVENTION: Ligands for
NUMBER OF SEQUENCES: 8
                                                                                                                                                                                                                                                                                   Query Match 100.0%; Score 1223; DB 10; Best Local Similarity 100.0%; Pred. No. 3.5e-110;
                                                                                                                                                                                                                                                                        Matches 231;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 24-JUN-1996
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/162,407
FILING DATE: December 3, 1993
APPLICATION NUMBER: 08/111,758
FILING DATE: August 25,1993
PRIOR APPLICATION DATA:
APPLICATION UMBER: 08/106,463
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/06,463
FILING DATE: August 12,1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/068,394
FILING DATE: May 24, 1993
CLASSIFICATION: 530
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SEQUENCE CHARACTERISTICS:
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181
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                                                                  121
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TELEFAX: (206) 233-0644
TELEX: 756822
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                ELPEPRPRQLLLLLLLPLTLVLLAAAWGLRWQRARRRGELHPGVPLPSHP
                                                                  LRFVQTNISHLLKDTCTQLLALKPCIGKACQNFSRCLEVQCQPDSSTLLPPRSPIALEAT 180
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                                                                                                                                     RESULT 11
US-09-448-378-2
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US-08-877-421-2
Sequence 2, Application US/09448378
GENERAL INFORMATION:
APPLICANT: Brasel, Kenneth
TITLE OF INVENTION: Dendritic Cell Stime
FILE REFERENCE: 2836-D
CURRENT APPLICATION NUMBER: US/09/448,378
CURRENT FILING DATE: 1999-11-23
NUMBER OF SEQ ID NOS: 2
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GENERAL INFORMATION:
APPLICANT: Winey, Joanne L.
APPLICANT: Mowatt, Allan McI.
APPLICANT: Abbott, Nicholas
TITLE OF INVENTION: A Method of Enhancing Antigen-Specific Peripheral Immune
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 100.0%; Score 1223; DB 12; Best Local Similarity 100.0%; Pred. No. 3.5e-110;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
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COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Macintosh 7.6
SOFTWARE: Microsoft Word, Version #6
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/877,421
FILING DATE: 17-JUN-1997
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Malaska, Stephen L.
REGISTRATION NUMBER: 32,655
REFERENCE/DOCKET NUMBER: 2855
TELECOMMUNICATION INFORMATION:
THE INFORMATION: NUMBER: 2855
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SEQUENCE CHARACTERISTICS:
LENGTH: 231 amino acids
TYPE: maino acid
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TELEFAX: 756822
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CITY: Seattle
STATE: Washington
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                                                                                                                                                                                                                                                                                                                                       61 VAVNLQDEKHCKALWSLFLAQRWIEQLKTVAGSKMQTLLEDVNTEIHFVTSCTFQPLPEC
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                                                                    Dendritic Cell Stimulatory Factor
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                                   RESULT 13
US-09-983-806-2
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   Sequence 2, Application US/09983806 GENERAL INFORMATION:
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; TYPE: PRT
; ORGANISM: Mus
US-09-448-378-2
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US-09-629-430B-8
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Best Local Similarity 100.0%;
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PRIOR FILING DATE: 1999-07-30
NUMBER OF SEQ ID NOS: 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/629,430B CURRENT FILING DATE: 2000-07-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: FLT-3-Ligand-Encoding Polynucleotide a TITLE OF INVENTION: Polynucleotide-Based Vaccine Enhancer FILE REFERENCE: 1530.0130001
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                 ELPEPRPRQLLLLLLLLPLTLVLLAAAWGLRWQRARRRGELHPGVPLPSHP 231
                                                                                           LRFVQTNISHLLKCTCTQLLALKPCIGKACQNFSRCLEVQCQPDSSTLLPPRSPIALEAT 180
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Pred. No. 3.5e-110;
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; TOPOLOGY: linear; MOLECULE TYPE: Protein; SEQUENCE DESCRIPTION: SEQ ID NO: US-09-983-806-2
                                   RESULT 14
US-10-095-449-2
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Sequence 2, Application US/10095449 GENERAL INFORMATION:
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Best Local Similarity
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INFORMATION FOR SEQ ID NO: 2:
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APPLICATION NUMBER: US/09/983,806
ETLING DATE: 25-Oct-2001
CLASSIFICATION: 530
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NAME: Malaska, Stephen L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                VAVNLQDEKHCKALWSLFLAQRWIEQLKTVAGSKMQTLLEDVNTEIHFVTSCTFQPLPEC 120
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                                                                                                                                     ELPEPRPRQLLLLLLLLPLTLVLLAAAWGLRWQRARRRGELHPGVPLPSHP 231
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Beckmann, M. Patricia
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                                                                                                                 ELPEPRPRQLLLLLLLPLTLVLLAAAWGLRWQRARRRGELHPGVPLPSHP 231
                                                                                                                                                                                             LRFVQTNISHLLKDTCTQLLALKPCIGKACQNFSRCLEVQCQPDSSTLLPPRSPIALEAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: August 25, 1993
APPLICATION NUMBER: 08/106,463
FILING DATE: August 12, 1993
APPLICATION NUMBER: 08/068,394
FILING DATE: May 24, 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US 08/162,407 FILING DATE: 03-DEC-1993 APPLICATION NUMBER: 08/111,758
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OPERATING SYSTEM: Macintosh 7.0.1
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TELEFAX: (206) 233-0644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/08/444,626
FILING DATE: 19-MAY-1995
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STREET: 51 University Street
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ilarity 100.0%;
Conservative 0
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INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
181 ELPEPRPROLLLLLLLLPLTLVLLAAAWGLRWQRARRRGELHPGVPLPSHP 231
                                                                               121 LRFVQTNISHLLKDTCTQLLALKPCIGKACQNFSRCLEVQCQPDSSTLLPPRSPIALEAT 180
                                                                                                     121 LREVQTNISHLLKDTCTQLLALKPCIGKACQNFSRCLEVQCQPDSSTLLPPRSPIALEAT 180
                                     181 ELPEPRPRQLLLLLLLPLTLVLLAAAWGLRWQRARRRGELHPGVPLPSHP 231
                                                                                                                                                                   61 VAVNLQDEKHCKALWSLFLAQRWIEQLKTVAGSKMQTLLEDVNTEIHFVTSCTFQPLPEC
                                                                                                                                                                                       61 VAVNLQDEKHCKALWSLFLAQRWIEQLKTVAGSKMQTLLEDVNTEIHFVTSCTFQPLPEC 120
                                                                                                                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                   1 MTVLAPAWSPNSSLLLLLLLLLSPCLRGTPDCYFSHSPISSNFKVKFRELTDHLLKDYPVT
                                                                                                                                                                                                                                                                                               1 MTVLAPAWSPNSSLLLLLLLLSPCLRGTPDCYFSHSPISSNFKVKFRELTDHLLKDYPVT 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: Apple Macintosh
operating SYSTEM: Macintosh 7.0.1
SOFTWARE: Microsoft Word, Version #5.1
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 98101
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: protein SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION: TELEPHONE: (206) 587-0430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Beckmann, M. Patricia
TITLE OF INVENTION: Ligands for flt3/flk-2 Receptors
NUMBER OF SEQUENCES: 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Lyman, Stewart
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: 08/111,758
FILING DATE: August 25, 1993
APPLICATION NUMBER: 08/106,463
FILING DATE: August 12, 1993
APPLICATION NUMBER: 08/068,394
FILING DATE: May 24, 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: 08/669,692
FILING DATE: 24-JUN-1996
APPLICATION NUMBER: US/08/162,407
FILING DATE: December 3,1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 231 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: (206) 587-04
TELEFAX: (206) 233-0644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Malaska, Stephen L
REGISTRATION NUMBER: 32,6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/10/095,449 FILING DATE: 13-Mar-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STATE: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 2813-C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Seattle
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Stephen L. Malaska, Immunex Corporation
                                                                                                                                                                                                                                                                                                                                                    100.0%;
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Pred. No. 3.5e-110;
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                                                                                                                                                                                                                                                                                                                                                                                 231;
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                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                   120
                                                                                                                                                                                                                                                     60
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US-60-368-263-2

Sequence 2, Application US/60368263 GENERAL INFORMATION:

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Qy
                                                                                                                                                                                                                                                                                                                                                                     ; APPLICANT: McKenna, Hilary J.
; APPLICANT: Liebowitz, David N.
; APPLICANT: Liebowitz, David N.
; APPLICANT: Maliszewski, Charles R.
TITLE OF INVENTION: METHODS OF USING FLT-3 LIGAND IN IMMUNIZATION PROTOCOLS
; FILE REFERENCE: 3399
; CURRENT APPLICATION NUMBER: US/60/368,263
; CURRENT FILING DATE: 2002-03-26
; NUMBER OF SEO ID NOS: 4
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 2
; SEQ ID NO 2
; SEQ ID NO 2
; TYPE: PRT
; ORGANISM: Mus sp
US-60-368-263-2
                                                                                                                                                    Qγ
                                                                                                                                                                                                              QΥ
Search completed: November 24, 2002, 10:17:26 Job time: 136.328 secs
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                                                                                                                                                                                  B
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                                                                                                                                                                                                                                                                        Qy
                                                                                                                                                                                                                                                                                                      Query Match 100.0%; Score 1223; DB 27; Length 231; Best Local Similarity 100.0%; Pred. No. 3.5e-110; Matches 231; Conservative 0; Mismatches 0; Indels 0;
                                                        Gaps
                                                                                                                                                                                                                                                                                                          0;
```

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GenCore version 5.1.3 Copyright (c) 1993 - 2002 Compugen Ltd
```

OM protein - protein search, using sw model

900 November 24, 2002, 10:08:46; Search time 14.6245 Seconds (without alignments)
1544.781 Million cell updates/sec

US-09-448-378-1 1242

Title: Perfect score:

1 MTVLAPAWSPTTYLLLLLLL......RPGEQVPPVPSPQDLLLVEH 235

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB DB seq length: 0 length: 2000000000

Post-processing: Minimum Match 0% Maximum

Maximum Match 100% Listing first 45 su

summaries

4321 pir1:\*
pir2:\*
pir3:\*

Database

<u>..</u>

PIR\_73:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	11	10	9	89	7	6	5	4	ω	2	_	NO.	Result
82.5	N	83	w	83.5	84	84	85	85	86	86	86	86.5	87	87.5	88	88.5	88.5	89	89	89.5	92	93	•		768.5	834	864.5	1242	Score	ı
6.6									6.9					7.0	7.1	7.1	7.1	7.2	7.2	7.2	7.4	7.5	48.8		•	67.1	69.6	100.0	Match	
426	418	1509	530	199	757	263	366	289	746	485	299	590	910	479	753	1386	238	793	387	474	661	1217	220	220	231	178	245	235	Length	
Ν	N	ν	N	N	N	N	2	2	2	N	2	2	N	ب	N	N	N	μ.	N	N	L	N	N	N	N	ν	N	2	. B	
136948	T19800	T19486	A45690	E75630	A39283	T03162	A37374	A87646	T28004	A33647	T17832	A40437	A53137	A32290	JQ0532	T00257	AB1990	S60735	148201	T19543	TNBE12	T22672	I58343	S43291	A49265	139076	S43293	I38440	TD	
-		hypothetical prote	transactivator EBN	hypothetical prote	gamma-glutamyl car		G		prot	sur	hypothetical prote	glutamic acid-rich	tyrosine kinase re	protein-tyrosine-p			μ.	Ω	adhalin - golden h	hypothetical prote	74K alpha trans-in	hypothetical prote	flt3 ligand isofor		flt3/flk-2 ligand	Flt3 ligand altern	FLT3/FLK2 ligand (		Description	

γ Вb

121 61

RFVQTNISRLLQETSEQLVALKPWITRQNFSRCLELQCQPDSSTLPPPWSPRPLEATAPT ASNIQDEELCGGLWRLVLAQRWMERLKTVAGSKMQGLLERVNTETHFVTKCAFQPPPSCL 120

180

	hypothetical prote	T13592	۵	1306	6.5	80.5	45
	hypothetical prote	T49482	2	1176	6.5	80.5	44
	class I cytokinase	JW0047	Ν	636	6.5	80.5	43
1	Ig epsilon chain C	EHHU	Ц	428	o.5	81	42
	probable transposa	S15591	2	388	6.5	81	41
	hypothetical prote	AI2016	N	294	6.5	81	40
	cysteine-rich exte	A48232	N	209	6.5	81	39
	cysteine-rich exte	B48232	N	196	6. 5	81	38
	related to cytoske	T50995	2	1119	6.6	81.5	37
	hypothetical prote	T13593	2	958	6.6	81.5	36
	stromelysin 3 (EC	S13423	2	488	6.6	81.5	35
	hypothetical prote	C75460	N	485	6. 6	81.5	34
	hypothetical prote	T23837	N	854	6.6	82	ω
	proline/leucine-ri	T06479	ν	106	6.6	82	32
	activin receptor p	JQ1484	N	513	6.6	82.5	31
	activin receptor i	D40829	N	512	6.6	82.5	30

## ALIGNMENTS

A; Molecule type: mRNA
A; Residues: 1-71,/A/,73-235 <HAN>
A; Residues: 1-71,/A/,73-235 <HAN>
A; Cross-references: GB:U04806; NID:9483844; PIDN:AAA17999.1; PID:9483845
A; Note: the authors translated the codon AGT for residue 25 as Met
C; Genetics: A.Molecule type: DNA
A.Residues: 1-235 <RE2>
A.Residues: 1-236 <RE2>
A.Cross-references: EMBL:U29874; NID:g1072036; PIDN:AAA90949.1; PID:g1072037
A.Cross-references: EMBL:U29874; NID:g1072036; PIDN:AAA90949.1; PID:g1072037
A.C.; Culpepper, J.; Campbell, D.; McClanahan, T.; Zurawski, S.; Bazan, J.F.;
felt, A.; Muench, M.; Kelner, G.; Namikawa, R.; Rennick, D.; Roncarolo, M.G.; Zlotnik
Nature 368, 643-648, 1994
A.Title: Ligand for FLT3/FLK2 receptor tyrosine kinase regulates growth of haematopoi
A.Reference number: S43290; MUID:94195428; PMID:8145851
A.Roccession: S43292
A.Status: preliminary A;Cross-references: EMBL:U03858; NID:g494978; PIDN:AAA19825.1; PID:g494979 R;Lyman, S.D.; Stocking, K.; Davison, B.; Fletcher, F.; Johnson, L.; Escoba Oncogene 11, 1165-1172, 1995 A;Title: Structural analysis of human and murine flt3 ligand genomic loci. A;Reference number: 139075; MUID:96032581; PMID:7566977 A;Accession: 139075 C;Date: 29-May-1990 #sequence\_revision 29-May-1998 #text\_change 01-Dec-2000 C;Accession: 138440; 139075; S43292 R;Lyman, S; D; James, L; Johnson, L; Brasel, K.; de Vries, P.; Escobar, S.S.; Downe Blood 83, 2795-2801, 1994 A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: mRNA A;Residues: 1-235 <RES> A;Title: Cloning of the human homologue of the murine flt3 ligand: a growth factor fo A;Reference number: I38440; MUID:94235842; PMID:8180375 A;Accession: I38440 C; Species: Homo sapiens (man) Qy В Qy A; Introns: 11/3; 48/3; 66/3; 114/3; 161/1; 220/3 A; Status: preliminary; translated from GB/EMBL/DDBJ flt3 ligand - human Query Match Best Local Matches 61 Local Similarity ASNLQDEELCGGLWRLVLAQRWMERLKTVAGSKMQGLLERVNTEIHFVTKCAFQPPPSCL 120 235; Conservative 100.0%; S 100.0%; P ative 0; Score 1242; DB 2; Pred. No. 5.4e-99; 0; Mismatches 0; Indels Length 235; 0, Gaps Escobar, 0, Ś

60

receptor:

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Holl

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Bb
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                                  δÃ
                                                                                                                                                                                                                                                                                                                                                                                     C:Species: Homo sapiens (man)
C:Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 21-Jul-2000
C:Accession: I39076
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nature 368, 643-648, 1994

A.Title: Ligand for FLTD/FELKZ receptor tyrosine kinase regulates growth of haematopoieti A; Reference number: $43290; MUID:94195428; PMID:8145851

A.Rocession: $43293
                                                                                                                                                           C; Genetics:
A; Introns:
                                                                                                                                                                                                    A; Cross-references:
                                                                                                                                                                                                                     A;Status: preliminary; translated A;Molecule type: DNA A;Residues: 1-178 <RES>
                                                                                                                                                                                                                                                                                                A; Title: Structural analysis of human and murine flt3 ligand A; Reference number: 139075; MUID:96032581; PMID:7566977
                                                                                                                                                                                                                                                                                                                                             R;Lyman, S.D.; Stocking, K.; Davison, B.; Fletcher, F.; Johnson, Oncogene 11, 1165-1172, 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                        Flt3 ligand alternatively spliced isoform - human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QУ
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A; Note: the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: mRNA
A; Residues: 1-245 <HAN>
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                                                                          Matches 160;
                                                                                                                                                                                 Genetics:
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  181 APQP------PLLLLLLPVGLLLLAAAWCLHWQRTRRRTPRPGEQVPPVPSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121
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    #TVLAPAWSPTTYLLLLLLLSGLSGTQDCSFQHSPISSDFAVKIRELSDYLLQDYPVTV 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPRPHPGEDTEAHRGESP---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RFVQTNISRLLQETSEQLVALKPWITRQNFSRCLELQCQPDSSTLPPPWSPRPLEATAPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ASNLQDEELCGGLWRLVLAQRWMERLKTVAGSKMQGLLERVNTEIHFVTKCAFQPPPSCL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RFVQTNISRLLQETSEQLVALKPWITRQNFSRCLELQCQPGA---PRPQSPGPAACGALT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ASNLQDEELCGALWRLVLAQRWMERLKTVAGSKMQGLLERVNTEIHFVTKCAFQPPPSCL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MTVLAPAWSPTTYLLLLLLLSSGLSGTQDCSFQHSPISSDFAVKIRELSDYLLQDYPVTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APQPPLLLLLLPVGLLLLAAAWCLHWQRTRRRTPRPGEQVPPVPSPQDLLLVEH 235
                                                                                                                                                     11/3; 48/3; 66/3; 114/3; 161/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   176;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APQPPLLLLLLPVGLLLLAAAWCLHWQRTRRRTPRPGEQVPPVPSPQDLLLVEH
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                                                                                             Similarity
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                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                              EMBL:U29874; NID:g1072036;
                                                                                           67.1%;
100.0%;
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73.0%;
                                                                        0;
                                                                                         Score 834; I
Pred. No. 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 864.5; 1
Pred. No. 1.2e
7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7;
                                                                                                                                                                                                                                                         from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           codon AGT for residue 25 as
                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -ARGCIAWTQRKLARGRSLPWAPLIPSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1.2e-66;
hes 27;
                                                                                                               DΒ
                                                                                           .3e-64;
                                                                                                                                                                                              PIDN: AAA90950.1;
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                                                                      0;
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                                                                                                                                                                                           PID:g1072038
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A;Molecule type: DNA
A;Residues: 1-197,'L',198-231 <RE2>
A;Cross-references: EMBL:U29875; NID:g1072039; PIDN:AAA90951.1; PID:g1072040
R;Hannum, C.; Culpepper, J.; Campbell, D.; McClanahan, T.; Zurawski, S.; Bazan, J.F.;
felt, A.; Muench, M.; Kelner, G.; Namikawa, R.; Rennick, D.; Ronçarolo, M.G.; Zlotnik
Nature 368, 643-648, 1994
A;Title: Ligand for FLT3/FLK2 receptor tyrosine kinase regulates growth of haematopoi
A;Reference number: S43290; MUID:94195428; PMID:8145851
A;Acteresion: S43290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R.Tyman, S.D.; Stocking, K.; Davison, B.; Fletcher, F.; Johnson, L.; Escobar, Oncogene 11, 1165-1172, 1995
A;Title: Structural analysis of human and murine flt3 ligand genomic loci. A;Reference number: 139075; MUID:96032581; PMID:7566977
A;Accession: 149447
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-163,'G',165,'HYAG' <RES>
A;Cross-references: EMBL:079875; NID:g1072039; PIDN:AAA90952.1; PID:g1072041
A;Accession: 149346
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A; Residues: 1-197, 'L', 198-231 <HAN>
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C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 08-Oct-1999
C;Accession: A49265; I49347; I49346; S43290
R;Lyman, S.D.; James, L.; Vanden Bos, T.; de Vries, P.; Brasel, K.; Gliniak, D.; Williams, D.E.; Beckmann, M.P.
Cell 75, 1157-1167, 1993
                                                                                                                                                                                                                                                                                                                                                                        C; Keywords: transmembrane
                                                                                                                                                                                                                                                                                                                                                                                              A; Introns: 11/3; 49/3; 67/3; 115/3; 164/1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Note: the sequence from Fig. 2c is inconsistent with
                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Experimental source: clone T110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Title: Molecular cloning of a ligand for the flt3/flk-2 tyrosine kinase A;Reference number: A49265; MUID:94084791; PMID:7505204
A;Accession: A49265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: GB:L23636; NID:g439441; PIDN:AAA39436.1; R;Lyman, S.D.; Stocking, K.; Davison, B.; Fletcher, F.; John:
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A; Residues: 1-231 <LYM>
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                                                                    LRFVQTNISRLLQETSEQLVALKPWITR--QNFSRCLELQCQPDSSTLPPPWSPRPLEAT 177
APTAPQPP--LLLLLLEPVGLLLLAAAWCLHWQRTRRTPRPGEQVPPVPSP 227
                                                                                                                                            VASNLQDEELCGGIJWRLVLAQRWMERLKTVAGSKMQGLLERVNTEIHFVTKCAFQPPPSC 119
                                        LRFVQTNISHLLKDTCTQLLALKPCIGKACQNFSRCLEVQCQPDSSTLLPPRSPIALEAT
                                                                                                                         VAVNLQDEKHCKALWSLFLAQRWIEQLKTVAGSKMQTLLEDVNTEIHFVTSCTFQPLPEC
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70.3%;
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                                                                                                                                                                                                                                                                                                             Score 768.5; DB Pred. No. 1.8e-58
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PLT3/FLK2 ligand (clone Til8) - mouse
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 20-Oct-1994 #sequence_revision 10-Nov-1995 #text_change 17-Mar-1999
C;Accession: S43291
R;Hannum, C.; Culpepper, J.; Campbell, D.; McClanahan, T.; Zurawski, S.; Bazan, felt, A.; Muench, M.; Kelner, G.; Namikawa, R.; Rennick, D.; Roncarolo, M.G.; Zl
Nature 368, 643-648, 1994
A;Title: Ligand for FLT3/FLK2 receptor tyrosine kinase regulates growth of haema
A;Reference number: S43290; MUID:94195428; PMID:8145851
A;Accession: S43291
A;Molecule type: mRNA
A;Residues: 1-220 <HANN
                                                                                                                                                                                                                                                                                                                                                                         flt3 ligand isoform 5H - mouse
C;Species: Mus sp. (mouse)
C;Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 05-Nov-1999
C;Accession: I58343
R;Lyman, S.D.; James, L.; Escobar, S.; Downey, H.; de Vries, P.; Brasel, K.;
Oncogene 10, 149-157, 1995
A;Title: Identification of soluble and membrane-bound isoforms of the murine A;Reference number: I58343; MUID:95124710; pMID:7824267
A;Accession: I58343
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A;Cross-references: GB:S76459; NID:g913479; PIDN:AAB33069.1; PID:g913480
                                                                                                                                                                                                                                                                                                                      A; Molecule type: mRNA
A; Residues: 1-220 < RES>
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                                   LRFVQTNISRLLQETSEQLVALKPWITR--QNFSRCLELQCQPDSSTLPPPWSPRP---- 173
                                                                                                            VASNLQDEELCGGLWRLVLAQRWMERLKTVAGSKMQGLLERVNTEIHFVTKCAFQPPPSC 119
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LRFVQTNISHLLKDTCTQLLALKPCIGKACQNFSRCLEVQCQPGNG---
                                                                         VAVNLQDEKHCKALWSLFLAQRWIEQLKTVAGSKMQTLLEDVNTEIHFVTSCTFQPLPEC 120
                                                                                                                                                  MTVLAPAWSPNSSLLLLLLLLSPCLRGTPDCYFSHSPISSNFKVKFRELTDHLLKDYPVT 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LREVQTNISHLLKDTCTQLLALKPCIGKACQNESRCLEVQCQPGNG-----GPRAQHHG 174
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61.5%;
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; Pred. No. 1.3e-44;
18; Mismatches 43
                                                                                                                                                                                                                                             Score 606.5;
Pred. No. 1.3
                                                                                                                                                                                                                             Mismatches
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C; Accession: C27342
R; Davison, A.J.; Scott, J.E.
J. Gen. Virol. 67, 1759-1816, 1986
J. Title: The complete DNA sequence of varicella-zoster A; Reference number: A27345; MUID:86306657; PMID:3018124
A; Accession: C27342
                                                                                                                                                                                                                                                                   A; Gene: 12
C; Superfamily: herpesvirus 77K alpha trans-inducing protein
C; Keywords: trans-inducing protein; transcription regulation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TNBE12
74K alpha trans-inducing protein - human herpesvirus 3
74K alpha trans-inducing protein - human herpesvirus 3
C:Species: human herpesvirus 3, varicella-zoster virus
C:Species: 30-Sep-1988 #sequence_revision 30-Sep-1988 #text_change 16-Jul-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    submitted to the EMBL Data Library, A; Reference number: Z19597
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R;Barlow, K.
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A; Introns: 742/2; 826/1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Experimental source: clone C; Genetics:
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A; Residues: 1-1217 <WIL>
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                                                                                                                                                                                                                                                                                                                                                                                                 A; Cross-references: EMBL: X04370; NID: g59989;
                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: DNA
A; Residues: 1-661 <DAV>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: EMBL:Z81548; NID:e1062020; PIDN:CAB04464.1; GSPDB:GN00021; CESP:FA;Experimental source: clone F54F12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Status: preliminary; translated
                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            743 GAVGGLLVVAIIGVILFFVFFQKKKKKEDKPDD--PPAPLP 781
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              627 MDAVKAVDGTKYSSVIDALEKLSTMDLDFQKYKFKEAPATLKAMDL----FFASYASNLA 682
                                                                                                                                                  19
                                                                                                79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity es 38; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LPVGLLLLAA-----AWCLHWQRTRRRTPRPGEQVPPVPSP 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATRITATALLTVCPGLLLPLVGTSHMFFLPYFLSFLSS
                                                                                                                                                LLSSGLSGTQDCS----FQHSPISSDFAVKI--RELSDYLLQDYPVTVASNLQDEELCG- 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MERLKTVAGSKMQGL---LERVNTEIHFVTKCAFQPPPSCLRFVQTNISRLLQETSEQLV 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ---LEATAPTAPQPPLLL-----LLLLPVGLLLLAA
GLW-WVYENTYWQYLKYTTGAEVPVTSEKVNKKSKSTVLLFSSVVANKPISRHPFKSKVI
                                               GLWRLVLAQRWMERLKTVAGSKMQGLLERVN----TEIHFVTKCAFQP---PPSCLRFV 123
                                                                                                LTSPVLQSTERHSVLLGLHHNNVPESLVVSCMSNDVHDGFMQRYMETIQRCLDDLKLSGD 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ALRPOPTTSDPTAAAPVPIPNNKGSLNGNPSPSSPPLLPPVASSTPAATPEESNMLLYII 742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ALKPWITRQNFSRCLELQCQPDSSTL---PPPWSPRPLEATAPTAP-----QPPLLLLLL 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  T22672
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                                                                                                                                                                                                 Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7.5%;
                                                                                                                                                                                                                      7.48;
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                                                                                                                                                                                                    29;
                                                                                                                                                                                                                    Score 92;
Pred. No. '
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Pred. No. 8;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GB/EMBL/DDBJ
                                                                                                                                                                                                                                              DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                   PIDN:CAA27895.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 2; Length 1217;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      201
                                                                                                                                                                                                 103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               68;
                                                                                                                                                                                                                                              Length 661
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                                                                                                                                                                                                 36;
                                                                                                                                                                                               Gaps
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  197
                                                                                                                                                                                                 11;
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A;Molecule type: mRNA
A;Residues: 1-387 <RES>
A;Cross-references: EMBL:U21677; NID:g726481; PIDN:AAA81645.1; PID:g726482
C;Superfamily: mouse adhalin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Вb
                                                                                                                                                     A;Title: Adhalin mrNA and cDNA sequence are normal in the cardiomyopathic hamster. A;Reference number: I48201; MUID:95278335; PMID:7758576
A;Accession: I48201
A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                         adhalin - golden hamster
C;Specites: Mesocricetus auratus (golden hamster)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 20-Jun-2000
C;Accession: I48201
R;Roberds, S.L.; Campbell, K.P.
FEBS Lett. 364, 245-249, 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross references: EMBL:Z82259; PIDN:CAB05129.1; GSPDB:GN00022; CESP:C28D4.2 A;Experimental source: clone C28D4 C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R;McMurray, A.
submitted to the EMBL Data Library, November 1996
A;Reference number: 219139
A;Accession: T19543
A;Status: preliminary; translated from GB/EMBL/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ъ
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A; Introns: 26/3; 72/3; 118/2; 169/1; 203/2; 240/2; 262/3; 298/3; 342/2; 391/3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: DNA
A; Residues: 1-474 <WIL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   T19543
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Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 7.2%; Score 89.5; D) Best Local Similarity 24.1%; Pred. No. 5.5; Matches 59; Conservative 29; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    267 ITVAQ 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              230 LLLVE 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        223 PKEPQ----
                                                                                                                                                                                                                                                                                                                                                                                                                     10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     248 GYGWMLWFLDVVD-----ARVCRHLKLQFRRIRGPRASV----IPDDLL 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             183 QPPLLLLLLPVGLLLLAAAWCLHWQRTRRRTPRPGEQVPPVPSPQDLL 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            77 VLAQRWMERLKTVAGSKMQGLLERVNTEIHFVTKCAFQPPPSCLR-FVQTNISRLLQET- 134
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VFTLLSERNLGPKMLGVFPGGRFEQFIPSRALQCLEISKPGLSKLIAPIVARVHTLDAPI 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TQDC-----SFQHS-PISSDFAVKIREL-SDYLLQDYPVTVASNLQDEELCGGLWRL 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -----SEQLVALKPWITRQNFSRCLELQC----QPDSSTLPPPWSPR--PLEATA 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VKIEEF--RIRAITGG-MSNLLFLVELPAH-LTPIQMEPEKALLRVHCQSDIDQLLSESV 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NSDYRGICQELREALGAVQKYM---YFMR------PDDPTNPSPDTRIRVQETAAYTAT 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ---TLQTARQWLERF----KKTPAGERPIEMYLTQAKVPKSDYPST 266
         7.2%;
23.4%;
      Score 89; DB 2; Pred. No. 4.8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 2; Length 474;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      82;
                           Length 387;
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Qy       4 LAPAWSPTTYLLLLLLSSGLSGTQDCSFQHSPISSDFAVKIRELSDYLLQDYPVTVASN 63         LII	RESULT 11  S60735  splicing factor SF3a 120K chain - human C:Species: Homo sapiens (man) C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 21-Jul-200 C;Accession: S60735; S60733 R:Kraemer, A.; Mulhauser, F.; Wersig, C.; Groening, K.; Bilbe, G. A;Title: Mammalian splicing factor SF3a120 represents a new member of the A;Reference number: S60733; MUID:96079958; PMID:7489498 A;Accession: S60735 A;Status: nucleic acid sequence not shown A;Molecule type: mRNA A;Residues: 1-793 <kra> A;Cross-references: EMBL:X85237; NID:g899297; PIDN:CAA59494.1; PID:g899298 A;Accession: S60733 A;Molecule type: protein A;Residues: 51-62:82-94;270-275;397-414;448-463 <kra2> C;Genetics: A;Gene: GDB:SF3A120; PRP21; SAP114 A;Cross-references: GDB:9955873 A;Map position: 22q12.1-22qter C;Superfamily: human splicing factor SF3a 120K chain; ubiquitin homology C;Keywords: pre-mRNA splicing G;Keywords: pre-mRNA splicing C;Keywords: pre-mRNA s</kra2></kra>	Matches 71; Conservative 26; Mismatches 97; Indels 110; Gaps  Oy 11 TTYLLLLLISGLSGTQDCSFQHSPISSDFAVKIRELSDYLLQDYPYTVASNLQDEELC 70  II
_	-Jul-2000 ; of the SURP fa :g899298 :g899298	ω

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DNA Res. 4, 345-349, 1997
A;Title: Characterization of cDNA clones in size-fractionated cDNA libraries from human A;Reference number: Z14085; MUID:98116662; PMID:9455484
   В
                                     Q
                                                                                                                                                                                                                             A;Status: preliminary; translated from GB/EMBL/DDBJA;Molecule type: mRNAA;Residues: 1-1386 <SEK>
                                                                                                                                                                                                                                                                                                                                                                               C;Species: Homo sapiens (man)
C;Date: 01-Feb-1999 #sequence_revision 01-Feb-1999 #text_change 21-Jul-2000
C;Accession: T00257
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A;Residues: 1-238 <KUR>
A;Cross references: GB:BA000019; PIDN:BAB77837.1;
A;Experimental source: strain PCC 7120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120 C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 30-Jun-2002 C;Accession: AB1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Qγ
                                                                                                                                                                                       A; Experimental source:
                                                                                                                                                                                                           A; Cross-references: EMBL: AB007945;
                                                                                                                                                                                                                                                                                                                                                                                                                                      hypothetical protein KIAA0476 - human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Reference number: AB1807; A; Accession: AB1990
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA
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                                                                                                                                                                                                                                                                                                                                         ;Seki, N.; Ohira, M.; Nagase,
NA Res. 4, 345-349, 1997
                                                                            Matches
                                                                                                                Query Match
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Best Local Similarity
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   1104
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                                                                                                                                                      KIAA0476
   SAGASGSKDAPVPGGP
                                   SSGLSGTQDCSFQHSPISSDFAVKIRELSDYLLQDYPVTVASNLQDEELC----GGLWRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GLLLLAAAWCLHWQRTRRRTPRPGEQVPPVPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LVALKPWITRQNFSRCLELQCQPDSSTLPPPW----SPRPLEATAPTAPQPPLLLLLLLPV 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DDDDTDISPGISTEV----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GSKMQGLLERVNTEIHFVTKCAFQPPPSCLRFVQTNISRLLQ------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MPRPPMASVVRLPPGSVIAPMPPIIHAPRINVVPMPPSAPPIMAPRPPPMIVPTAFVPAP 656
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APQPPLLLLLLPVGLLLLAAAWCLHWQRTR-----RRTPRPGEQVPP---VPSP 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PQSLKP--TKPIPPKLIEPKKSEDSKNLQRPRIPDSPKPIKNSQPEAPKPV--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HSKKTTTYYESINEVCNQYLKSYEKKPLVII-----QILG--W----SQRLMRYYKTVD 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N.; Shimpo, S.
205-213, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             44;
                                                                         Similarity 23.:
53; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7.1%; 20.8%;
                                                                                              7.1%;
23.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -EPPKPWERVPKKPS
                                                                                                                                                                                                                                                                                                                                                         T.;
                                                                           28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Score 88.5; D; Pred. No. 3; 32; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           32;
                                                                         Score 88.5; I
Pred. No. 23;
28; Mismatches
                                                                                                                                                                                                                                                                                                                                                   Ishikawa, K.; Miyajima, N.; Nakajima, D.; Nomura,
                                                                                                                                                                                                       NID:g3413913; PIDN:BAA32321.1; PID:g3413914
-GPVLSDRRLCLA--LDEPQLCNGHMGGASRR 1148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -VVRKIPKVIETPKIVKPQKTEDIKTLES 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   237
                                                                                                                DΒ
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                                                                                                            Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 238;
                                                                           Indels
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                                                                         63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       77;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GSPDB:GN00179
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                                                                       Gaps
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A;Molecule type: mRNA
A;Residues: 1-227,'A',229-479 <JIM>
A;Cross-references: EMBL:X57495; NI
                                                                                        R;Jimenez, J; Alphey, L.; Nurse, P.; Glover, D.M. EMBO J. 9, 3565-3571, 1990
A;Title: Complementation of fission yeast cdc2(ts) and A;Reference number: S12008; MUID:91006056; PMID:2120044
                                                                                                                                                                                                                                                A; Title: Genetic control of cell division patterns in the A; Reference number: A32290; MUID:89195217; PMID:2702688 A; Accession: A32290
                                                                                                                                                                                                                                                                                                                      R;Edgar, B.A.; O'Farrell, P.H.
Cell 57, 177-187, 1989
                                                                                                                                                                                                                                                                                                                                                                protein-tyrosine-phosphatase (EC 3.1.3.48) cdc25 homolog string - fruit fly (Drosophi
C;Species: Drosophila melanogaster
C;Date: 05-Oct-1989 #sequence_revision 25-Apr-1997 #text_change 11-Jun-1999
C;Accession: A32290; S12008
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R;Ding, S.; Keese, P.; Gibbs, A.
J. Gen. Virol. 71, 925-931, 1990
A;Title: The nucleotide sequence of the genomic RNA of kennedya
A;Reference number: JQ0532; MUID:90218040; PMID:2324710
A;Accession: JQ0532
                                                                A; Accession: S12008
                                                                                                                                                           A;Cross-references: GB:M24909; NID:g158507; PIDN:AAA28916.1; R;Jimenez, J.; Alphey, L.; Nurse, P.; Glover, D.M.
                                                                                                                                                                                                     A; Molecule type: mRNA
A; Residues: 1-479 <EDG>
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C:Species: Kennedya yellow mosaic virus
C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: GB:D00637; NID:g221969; PIDN:BAA00531.1; A;Experimental source: strain Jervis Bay isolate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C; Accession:
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JQ0532
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: mRNA
A; Residues: 1-753 <DIN>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              534 PPDVFHDCQPSSPTSHVVGYRRLLGSGISLPFKLAFW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              420 RLSTQPPSSPQTSSSPPPPSPRTDASGIQTPLASPPSKRKEKSLPHPSHQ----PPSHSK 475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100 RVNTEIHFVTKCAFQPPPSCLRF----VQTNIS-----RLLQETSEQLVALKPWITR 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 148 QNFSR----CLELQCQPDSSTLPPPWSPRPLEATAPTAPQPPLLLLLLLP---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RNLRRHSALPLLLPIHPTKTTQPHPAVPQP--TAGPTPHPPPTKKIPLHPPKSQERHPSP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19;
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NID:g7706; PIDN:CAA40732.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         58;
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                                                                                                                cdc25(ts) mutants identifies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
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PID:97707

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A;Gene: FlyBase:stg
A;Gene: FlyBase:stg
A;Cross-references: FlyBase:FBgn0003525
C;Function:
A;Description: catalyzes hydrolysis of peptidyl-phosphotyrosine to peptidyl-tyrosine and A;Description: catalyzes hydrolysis of peptidyl-phosphotyrosine to peptidyl-tyrosine and A;Pathway: initiation of mitosis
A;Note: cdc25 activates the cdc2 protein kinase by dephosphorylating it
C;Superfamily: protein-tyrosine-phosphatase string; cdc25-type protein-tyrosine-phosphat
C;Keywords: cell cycle control; mitosis; phosphoprotein; phosphoric monoester hydrolase;
F;352-456/Domain: cdc25-type protein-tyrosine-phosphatase homology <PTPD-
F;399/Active site: Cys (phosphocysteine intermediate) #status predicted
F;385/Binding site: substrate phosphate (Arg) #status predicted
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                                                                                                              243 VTISH 247
                                                                                                                                                                       231 LLVEH 235
                                                                                                                                                                                                                             200 ---TARDCFKRPEPP----
                                                                                                                                                                                                                                                                                174 LEATAPTA---POPPLILLILLIPVGLLLLAAAWCLHWQRTRRRTPRPGEQVPPVPSPQDL 230
                                                                                                                                                                                                                                                                                                                                            147 SGLN-----SLISGQIKEQPAAKSPAGLSMRRPSVRRCLSMTESNTNSTTTPPPKTPE- 199
                                                                                                                                                                                                                                                                                                                                                                          118 SCLRFVQTNISRLLQETSEQLVALKP---WITRQNFSRCLEL-QCQPDSSTLPPPWSPRP 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                        118 CSMESSMDDE------P 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               58 VTVASNLQDEELCGGLWRLVLAQRWMERLKTVAGSKMQGLLERVNTEIHFVTKCAFQPPP 117 : | : | : | : |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          72 MGLLSPEGSPQRFQIVRQPKILPAMGVSS-----DHTPARS-FRI-FNSLSS-----T 117
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Title:
Perfect score:
Sequence:
Database :
                                   Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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Gapop 10.0 , Gapext 0.5
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1242
1 MTVLAPAWSPTTYLLLLLLL.....RPGEQVPPVPSPQDLLLVEH 235
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SwissProt_40:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

33 33 33 33	1 1 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	Result
80.5 80 80 80 80 80	1242 768 89.5 89.5 89.5 89.5 87.5 87.5 87.6 87.6 86.8 87.6 86.8 87.8 86.8 87.8 88.8 81.5 81.5 81.5	Score
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hepatitis b	homo sapien	c fatty aci	vibrio chol	mus musculu	synechocyst	homo sapien	h epithelia	oryctolagus	rattus norv	homo sapien	saccharomyc

## ALIGNMENTS

X-RA MEDL Sacva "Fit bund Nat.	RP SEQUENCE FROM N.A. RX MEDLINE=94235842; Pu RX Lyman S.D., James L. RA Lyman S.D., James L. RA Escobar S.S., Downey RT "Cloning of the huma RT factor for early her RT Blood 83:2795-2801(1 RN [3] RP SEQUENCE FROM N.A., RX MEDLINE=96032581; Pu RA Lyman S.D., Stocking RA Escobar S.; RT Oncogene 11:1165-117		SULT 1  3L_HUMAN  FL3L, HUMAN  P49771;  01-OCT-199  01-OCT-199  15-JUN-200  SL cytokin  11gand) (F  FLT3LG.  Homo sapie  Eukaryota;  Mammalia;  NCBI_TaxIC
APHY   PubMa One T Cture cture ne kno NI ST NI S	PubMed=81803 L. Johnson L. Johnson ney H. Splet uman homologu hematopoletic 1(1994), AND ALTERN PubMed=75669 ing K., Davis sis of human 1172(1995).	DM N.A 95428; Pulpep Kaste Kaste (kaste	RD; Creat Last Last (Fms. hordat
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lities of helical EARLY HEMATOPOIETIC THER COLONY STIMULATING tein (isoform 1); brane-bound (shown here) e splicing.	gand: a growth  mcKenna H.J.; gand: a growth  nson L., genomic loci.";	Zurawski S., n J., Luh J., A., olo M.G., F.; tes growth of NAS.";	3 ligand) (Flt3 Euteleostomi;

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RESULT 2
F13L_MOUSE
ID F13L_M
AC P49772
DT 01-OCT
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DE SL Cyt
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                                                                                  FL3L_MOUSE STANDARD: PRT; 232 AA.
P49772; Q64085;
01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
SL cytokine precursor (Fms-related tyrosine Kinase ligand) (FL5L).
FLT3LG OR FLT3L.
SEQUENCE FROM N.A.
MEDLINE=94195428; PubMed=8145851;
                                                Eukaryota; Metazoa;
Mammalia; Eutheria;
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                                                                        Mus musculus (Mouse)
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Pfam; PF02947; flt3_lig; 1.
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EMBL; U03858; AAA19825.1; --
EMBL; U29874; AAA90949.1; --
EMBL; U29874; AAA90950.1; --
PDB; 1ETE; 09-JUN-00.
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Rodentia;
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N-LINKED (GLCNAC. ..) (POTENTIAL).
DSSTLPPWSRRPLEATA -> VETVFHRVSQDGLDLLTS
(IN ISOFORM 2).
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SL CYTOKINE.
EXTRACELLULAR (POTENTIAL).
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Sciurognathi;
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Pred. No. 1.1e-96;
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CYTOPLASMIC (POTENTIAL).
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EMBL; U04807; AAA18000.1; --
EMBL; L23636; AAA39436.1; --
EMBL; U29875; AAA90952.1; --
EMBL; U29875; AAA90952.1; --
EMBL; S76459; AAB33069.1; --
EMBL; S76464; AAB33070.1; --
EMBL; U44024; AAA93307.1; --
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"Identification of soluble and membrane-bound isoforms flt3 ligand generated by alternative splicing of mRNAs. Oncogene 10:149-157(1995).
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[3]
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Lyman S.D., James L., Vandenbos T., Devries P., Brasel K.,
Gliniak B., Hollingsworth L.T., Picha K.S., McKenna H.J.,
Splett R.R., Fletcher F.A., Maraskovsky E., Farrah T.,
Foxworthe D., Williams D.E., Beckmann M.P.;
"Molecular cloning of a ligand for the flt3/flk-2 tyrosine kinase
receptor: a proliferative factor for primitive hematopoietic cells.";
Call 75:1157-1167(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING. MEDLINE-95124710; PubMed=7824267; Lyman S.D., James L., Escobar S., Downey H., Brasel K., Stocking K., Beckmann M.P., Copela
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[2]
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SUBBURIT: Homodimer (soluble isoform) (By similarity).
SUBCELLULAR LOCATION: Type I membrane protein. Two sol isoforms are also produced by alternative splicing. On isoform 3/E6, is biologically active, while the other, 4/E6Deltal6, is inactive.
ALTERNATIVE PRODUCTS: 4 isoforms; 1/6C (shown here), 2 and 4/E6Deltal5; are produced by alternative splicing.
                                             MGI:95560;
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                                                                                                                                                                                                                                                                             SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation een the Swiss Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way by non-profit institutions as long as its content is in no way.
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N.G.,
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Glycoprotein;

Transmembrane; Alternative splicing; Signal.

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       the European Bloinformatics Institute. There are no restrictions on its way non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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01-NOV-1990
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"The complete DNA sequence of varicella-zoster virus.";
J. Gen. Virol. 67:1759-1816(1986).
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Alphaherpesvirinae; Vari
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MEDLINE=86306657; PubMed=3018124;
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AR-1989 (Rel. 10,
OV-1990 (Rel. 16,
a trans-inducing
                                                                SWISS-PROT entry is copyright. It is produced through a collaboration sen the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                             LREVQTNISHLLKDTCTQLLALKPCIGKACQNFSRCLEVQCQPDSSTLLPPRSPIALEAT
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                                                                                                                                                                                                                                                                                                                                                                 ELPEPRPRQLLLLLLLLLPLTLVLLAAAWGLRWQRARRR----
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170
159
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                                                                                                 OF ALPHA GENES.
                                                                                                                                                                                                                                                                                                         STANDARD;
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ses, no RNA stage;
Varicellovirus.
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Last annotation updat
factor 74 kDa protein.
                                                                                                                                                                                                                                                                                    Created)
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VOCOP -> GLIMOATT
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N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
DSSTLLPPRSPIALEATELPEPRPRQLLLLLLLLLPTTVL
DSSTLLPPRSPIALEATELPEPRPRQPLPSHP -> GNGGPRAQH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A -> G (IN REF. 1).
MISSING (IN REF. 2).
; 3A3680D3CB69FBA6 CRC64;
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EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 768;
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CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LKMYLYV (IN ISOFORM 2)
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                                                                                                                                                                                                                                                                                                          661
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                                                                                                                                                                                                                Herpesviridae;
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                                                                                                                                                                                                                            (VZV)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 232;
                                                                                                                                                                                                                                                                                                                                                                 -GELHPGVPLP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                O75899; O75974; O75975; Q9UNS9; Q9UNR1; Q9P1R2;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Gamma-aminobutyric acid type B receptor, subunit 2 precursor (GABA-B receptor 2) (GABA-B-R2) (Gb2) (GABABR2) (G protein-coupled receptor 51) (GPR 51) (HG20).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR005051; Herpes_UL46; 1.
Pfam; PF03387; Herpes_UL46; 1.
Transcription regulation; Trans-a
SEQUENCE 661 AA; 74272 MW; C5
                                                                                                                            Herzog H.; "Cloning and characterization of a novel human "Cloning and characterization of a novel human with high affinity for GABA and low affinity fo submitted (NOV-1998) to the EMBL/GenBank/DDBJ of the EMBL/GenBank/DD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            White J.H., Wise A., Main M.J., Green A., Fraser N.J., Disney G.H. Barnes A.A., Emson P., Foord S.M., Marshall F.H.; "Heterodimerization is required for the formation of a functional
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. (ISOFORM 2A)
TISSUE=Cerebellum;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GBR2_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; X04370; CAA27895.1; PIR; C27342; TNBE12.
                                                                                                                                                                                                                                                                                                       Clark J.A., Mezey E., Lam A.S., Bonner "Distribution of the GABA(B) receptor Erain Res. 860:41-52(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GABBR2 OR GPR51
                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE=Brain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GABA(B)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=99087321;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa;
  SEQUENCE
                                         Submitted
                                                            SEQUENCE FROM N.A. TISSUE-Hippocampus; Borowsky B., Laz T.
                                                                                                                                                                                                                                           Liu M.,
                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=20193514; PubMed=10727622;
                                                                                                                                                                                                                                                                                                                                                                                                                        PARTIAL SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Heterodimerization is required for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             198
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QTNISRLLQETSEQLVALKPWITRQNFSRCLELQCQPDSSTLPPPWSP-RPLEATAPTAP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QPPLLLLLLPVGLLLLAAAWCLHWQRTRRRTPRPGEQVPPVPSPQDLL
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                                                                                                                                                                                                                                         Parker R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         receptor
  FROM
                                       B., Laz T.,
(JAN-1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                        FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PubMed=9872316;
                                                                                                       (ISOFORM
                                                                                                                                                                                                                                         McCrea K.,
(ISOFORM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chordata;
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v., Watson
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2A)
                                         C.;
EMBL/GenBank/DDBJ
                                                                                                          2A)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 92;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C5CA77A16D365379
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                                                                                                                                                                                                                                                                                                                                                     Bonner T.I.;
                                                                                                                                                                                                                                         J.,
                                                                                                                                                                                                                                                                                                                                                                                                                        2A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           941
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J databases.
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                                                                                                                                                                                               GABA-B receptor subtype
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                                                                                                                                                                                                                                           Sutherland
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                                                                                                                                                                                                                                                                                                                                   CNS. ";
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                                                                                                                                                                                                                                           G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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Sullivan R., Chateauneuf A., Coulombe N., Kolakowski L.F. Jr., Johnson M.P., Hebert T.E., Ethier N., Belley M., Metters K., Abramovitz M., O'Neill G.P., Ng G.Y.K.; "Coexpression of full-length gamma-aminobutyric Acid(B) (GABA(B)) receptors with truncated receptors and metabotropic glutamate receptor 4 supports the GABA(B) heterodimer as the functional
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   J. Pharmacol. Exp. Ther. 293:460-467(2000)
-!- FUNCTION: RECEPTOR FOR GABA. THE ACTIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        receptor."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Identification of a GABAB receptor subunit, functional GABAB receptor activity.";
J. Biol. Chem. 274:7607-7610(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=99175124; PubMed=10075644;
Ng G.Y.K., Clark J., Coulombe N., Ethier N., Hebert T.E., Sullivan Kargman S., Chateauneuf A., Tsukamoto N., McDonald T., Whiting P., Mezey E., Johnson M.P., Liu Q., Kolakowski L.F. Jr., Evans J.F.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-99189236; PubMed-10087195;
Ng G.Y.K., McDonald T., Bonnert T., Rigby M., Heavens R., Whiting Chatteauneuf A., Coulombe N., Kargman S., Caskey T., Evans J.F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE=Fetal brain;
MEDLINE=99189236; Pu
Ng G.Y.K., McDonald
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mol. Cell. Neurosci. 13:180-191(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    expression and coupling
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. (ISOFORM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bonner T.I., O'Neill G.P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R1A-R2 INTERACTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GABABR1."
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            TISSUE SPECIFICITY: HIGHLY EXPRESSED IN BRAIN, ESPECIALLY IN CEREBRAL CORTEX, THALAMUS, HIPPOCAMPUS, FRONTAL, OCCIPITAL AN TEMPORAL LOBE, OCCIPITAL POLE AND CEREBELLUM, FOLLOWED BY COLCALLOSUM, CAUDATE NUCLEUS, SPINAL CORD, AMYGDALA AND MEDULLA WEAKLY EXPRESSED IN HEARY, TESTIS AND SKELETAL MUSCLE.

DOMAIN: ALPHA-HELICAL PARTS OF THE C-TERMINAL INTRACELLULAR INTERACTION WITH GABA-B RECEPTOR 1.

SIMILARITY: BELONGS TO FAMILY 3 OF G-PROTEIN COUPLED RECEPTOR

SIMILARITY: BELONGS TO FAMILY 3 OF G-PROTEIN COUPLED RECEPTOR
                                                                                                                                                                                                                               PRODUCED BY ALTERNATIVE SPLICING.
TISSUE SPECIFICITY: HTGHTY THE
                                                                                                                                                                                                                                                                                             HAPPEN.

SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MC
COEXPRESSION OF GABA-B-R1 AND GABA-B-R2 APPEARS TO
PREREQUISITE FOR MATURATION AND TRANSPORT OF GABA-B
PLASMA MEMBRANE.

ALTERNATIVE PRODUCTS: 3 ISOFORMS: 2A (SHOWN HERE),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUBUNIT: HETERODIMER OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INOSITOL PHOSPHOLIPIDS HYDROLYSIS. PLAYS A CRITICAL ROLE IN THE FINE-TUNING OF INHIBITORY SYNAPTIC TRANSMISSION. PRE-SYNAPTIC GABA-B-R INHIBIT NEUROTRANSMITER RELEASE BY DOWN-REGULATING HIGH-VOLTAGE ACTIVATED CALCIUM CHANNELS, WHEREAS POSTSYNAPTIC GABA-B-R DECREASE NEURONAL EXCITABILLITY BY ACTIVATING A PROMINENT INWARDLY RECTIFYING POTASSIUM (KIR) CONDUCTANCE THAT UNDERLIES THE LATE INHIBITORY POTSSYNAPTIC PRENTIALS. NOT ONLY IMPLICATED IN SYNAPTIC INHIBITION BUT ALSO IN HIPPOCAMPAL LONG-TERM POTENTIATION, SLOW WAVE SLEEP, MUSCLE RELAXATION AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FUNCTION: RECEPTOR FOR GABA. THE ACTIVITY OF THIS RECEPTOR IS MEDIATED BY G-PROTEINS THAT INHIBITS ADENYLYL CYCLASE ACTIVITY, STIMULATES PHOSPHOLIPASE A2, ACTIVATES POTASSIUM CHANNELS, INACTIVATES VOLTAGE-DEPENDENT CALCIUM-CHANNELS AND MODULATES INOSITOL PHOSPHOLIPIDS HYDROLYSIS. PLAYS A CRITICIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 56:288-295(1999).
   RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9
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SUBFAMILY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GABA-B-R1 AND GABA-B-R2. AND HOMODIMERIC ASSEMBLY
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GABA-B-R1
                                                       INTRACELLULAR REGION RECEPTOR 1.
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Pfam; PF01094; ANF_TECEPLOT; 1.

PROSITE; PS00979; G_PROTEIN_RECEP_F3_1; FALSE_NEG.

PROSITE; PS00980; G_PROTEIN_RECEP_F3_3; FALSE_NEG.

PROSITE; PS00981; G_PROTEIN_RECEP_F3_3; FALSE_NEG.
                                                            SEQUENCE
                                                                                                              VARIANT
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InterPro; IPR000337; GPCR_Mgr.
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                                                                                                                                                                                                                                                                                                                                                                                                                        Postsynaptic
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AF056085; AAC63228.1;
AF095723; AAC63383.1;
AF095724; AAC63384.1;
AF095724; AAC63384.1;
AF095784; AAD30389.1;
AF074483; AAD30338.1;
AF074483; AAD30338.1;
AF0749375; AAC99345.1;
AF069755; AAC99345.1;
AF0699033; AAD45867.1;
 SPRPLEATAPTAPQPP----LLLLLLLPVGLLLLAAAWCLHWQRTRRRTPRPGEQVPPV 224
                               Similarity
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G_PROTEIN_RECEP_F3_4;
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941
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                                                                                                                                                                                                                                                                                                                                                                                                                        ptor; Transmembrane;
Coiled coil; Alterna
                                        . 28;
                                                            WW.
                                                          /FTId=VAR_010149.
S -> R (IN REF. 5).
P -> R (IN REF. 5).
G -> E (IN REF. 3).
MW; 09F1773DB0673C5D C
                    Score 89.5; D
Pred. No. 6.4;
2; Mismatches
                     2;
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Y -> F.
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T -> A.
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CYTOPLASMIC (
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                                                                                                                                                                                                                                                                                                                                                                                         GAMMA-AMINOBUTYRIC ACID TYPE B RECEPTOR.
                                                                                                                                                                                                                                                                                                                                                                                                                     coil; Alternative splicing;
                                                                                                                                                                                                                                                                                 (POTENTIAL)
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(IN ISOFORM 2B).
VMVSGL -> TTLGRGVCCRNTVGSGCGEAGHHG
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GLCNAC . .)

GLCNAC . .)
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SGCA_MESAU
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Sakamoto A., Ono K., Abe M., Jasmin G., Eki T., Murakami Y.,

Masaki T., Toyo-oka T., Hanaoka F.;

"Both hypertrophic and dilated cardiomyopathies are caused by mut

of the same gene, delta-sarcoglycan, in hamster: an animal model

disrupted dystrophin-associated glycoprotein complex.";

Proc. Natl. Acad. Sci. U.S.A. 94:13873-13878(1997).
                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIGNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Alpha-sarcoglycan precursor (Alpha-SG) (Adhalin)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cytoskeleton;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This
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Q64255;
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                                                                                                                                                                                                  Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIMILARITY: BELONGS TO THE SARCOGLYCAN ALPHA/EPSILON FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FUNCTION: COMPONENT OF THE SARCOGLYCAN COMPLEX, A THE DYSTROPHIN-GLYCOPROTEIN COMPLEX WHICH FORMS A F-ACTIN CYTOSKELETON AND THE EXTRACELLULAR MATRIX. SUBCELLULAR LOCATION: Type I membrane protein. Sar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE SPECIFICITY:
                                  GGLWRL-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HEART MUSCLE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (Potential)
                                                                                                                 TTYLLLLLLSSGLSGTQDCSFQHSPISSDFAVKIRELSDYLLQDYPVTVASNLQDEELC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lett. 364:245-249(1995)
                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      non-profit institutions as long as its content is in no way and this statement is not removed. Usage by and for commercial requires a license agreement (See http://www.isb-sib.ch/announce/an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              glycoprotein) (50DAG)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Metazoa;
                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                         ; Transmembrane; 1 23 24 387 290 21 311 311 312 387 390 335 474 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BAA12025.1; -.
AAA81645.1; -.
                                                                                                                                                                                                                                                                    AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE=Heart muscle;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
---VLAQRWMERLKTVAGSKMQGLLERVNTEIHFVT-----
                                                                                                                                                                                                                                                                  43326
                                                                                                                                                                                             7.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chordata;
                                                                       EDPEGPRLPYQAEFLVRSHDVEEVL----PSTPANRFL--TAL 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRONGLY EXPRESSED
                                                                                                                                                                                                                                                                  MW;
                                                                                                                                                                                          Score 89; DB 1;
Pred. No. 2.6;
                                                                                                                                                                                                                                                     N-LINKED (GLCNAC. ..) (POTENTIAL)
N-LINKED (GLCNAC. ..) (POTENTIAL)
, D8599C0FAF646C3F CRC64;
                                                                                                                                                                                                                                                                                                                                    CYS-RICH.
                                                                                                                                                                                                                                                                                                                                                        CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                      EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                               POTENTIAL.
ALPHA-SARCOGLYCAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Craniata; Ver
Sciurognathi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   normal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    There are no restrictions ong as its content is in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Vertebrata;
thi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ĀΑ
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                                                                                                                                                                    97;
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                                                                                                                                                                                                                Length 387;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (50 kDa
                                                                                                                                                                    Indels 110;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A SUBCOMPLEX OF
A LINK BETWEEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Euteleostomi;
; Cricetinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               dystrophin-
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RESULT 6
S3A1_HUMAN
ID S3A1_H
XX MEDLING-20057165; PubMed=10591208;
RA Dunham I., Hunt A.R., Collins J.E., Bruskiewich R., Beare D.M.,
RA Clamp M., Smink L.J., Ainscough R., Almeida J.P., Babbage A.K.,
RA Bagguley C., Balley J., Barlow K.F., Bates K.N., Beasley O.P.,
RA Bird C.P., Blakey S.E., Bridgeman A.M., Buck D., Chen Y., Clark G.,
RA Burrill W.D., Burton J., Carder C., Carter N.P., Chen Y., Clark G.,
RA Clegg S.M., Cobley V.E., Cole C.G., Collier R.E., Connor R.,
Clark G., Collier R.E., Connor R.,
RA Clagg S.M., Cobley V.E., Cole C.G., Collier R.E., Connor R.,
RA Clamp D.D., Dockree C., Dodsworth S.J., Durbin R.M., Ellington A.G.,
RA Conroy D., Corby N.R., Coville G.J., Cox A.V., Durbin R.M., Ellington A.G.,
RA Clamp S.L., Fey J.M., Fleming K., French L., Garner A.A.,
Dhami P.D., Dockree C., Dodsworth S.J., Durbin R.M., Ellington A.G.,
RA Gibbert J.G.R., Goward M.E., Grafham D.V., Griffiths M.N.D., Hall C.,
RA Hall R.E., Hall-Tamlyn G., Heathcott R.M., HO S., Holmes S.,
RA Hunt S.E., Jones M.C., Kershaw J., Kimberley A.M., King A.,
RA Martyn I.D., Mashreghi-Mohammadi M., Matthews L.H., McCann O.T.,
RA Martyn I.D., Mashreghi-Mohammadi M., Matthews L.H., McCann O.T.,
RA McClay J., McClaren S., McMurray A.A., Milne S.A., Morttmore B.J.C.T.,
RA McClay J., McClaren S., McMurray A.A., Milne S.A., Morttmore B.J.C.T.,
RA McClay J., McClaren S., McMurray A.A., Milnes S.A., Morttmore B.J.C.T.,
RA Williams L., Walliams S.A., Walliamson H., Willey D.L.,
RA Williams L., Walliams S.A., Walliamson H., Willey D.L.,
RA Williams L., Walliams S.A., Walliamson H., Willey T.E., Wilming L.,
RA Williams L., Walliams S.A., Walliamson H., Willer T.E., Wilming L.,
RA Roe B.A., Chen F., Chu L., Crabtree J., Deschamps S., Do A., Do T.,
RA Roe B.A., Chen F., Chu L., Crabtree J., Deschamps S., Do A., Do T.,
RA Phan S., Ois S., Cian Y., Way L., Ren Q., Shaull S., Sloan D., Song L.,
RA Wang Q., Wang Y., Wang Z., White J., Wallingham D., Wu H., Yao Z.,
                 Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Db
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=96079958; PubMed=7489498;
Kraemer A., Mulhauser F., Wersig C., Groning K
"Mammalian splicing factor SF3a120 represents
SURP family of proteins and is homologous to t
factor PRP21p of Saccharomyces cerevisiae.";
PRP 1.260.372.1006
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Splicing factor 3 subunit 1 (Spliceosome associated protein 114) (SAP
114) (SF3a120):
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       S3A1_HUMAN
Q15459;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SF3A1 OR SAP114.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  162
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CAQGQPPLLSCYDSLAPHFRVDWCNVSLVDKSVPEPLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CAFQPPP--SC-----LRFVQTNISRLLQETSEQLVALKPWITRQNFSRCLELQCQPD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MATSDIQMVHHCTIHGNTEELRQMAARREVPRPLSTLPMFNVRTGERLPPRVDSAQVPLI 383
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GGLWELGELQLLNITSALDRGGRVPLPIEGRKEGVYIKVGSATPFSTCLKMVASPDSYAR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         793
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FUNCTIONAL ASSOCIATION Of U2 SNRNP with the ATP-independent RT spliceosomal complex E.";
RL Mol. Cell 5:779-787(2000).
RL Mol. Cell 5:791-787(2000).
RESEMBLY FORMED BY THE SPLICING FACTOR SF3A REQUIRED FOR THE SESENTIAL, IT MAY ANCHOR U2 SNRNP TO THE PRE-MRNA. MAY ALSO BE CELL COMPONENT OF SPLICING FACTOR SF3A WHICH IS COMPOSED OF THREE SUBUNITS: COMPONENT OF SPLICING FACTOR SF3A WHICH IS COMPOSED OF THREE SUBUNITS: SF3A3/SAP61, SF3A2/SAP62, SF3A1/SAP114. SF3A ASSOCIATES WITH THE SPLICING FACTOR SF3B AND A 12s RNA UNIT TO FORM THE U2 SMALL NUCLEAR RIBONUCLEOPROTEINS COMPLEX (U2 SNRNP).
CC INTERACTS WITH SF3A3.
CC INTER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 Zhan M., Zhang G., Chissoe S., Murray J., Miller N., Minx P.,
28 Fulton R., Johnson D., Bemis G., Bentley D., Bradshaw H., Bourne S.,
28 Cordes M., Du Z., Fulton L., Goela D., Graves T., Hawkins J.,
28 Hinds K., Kemp K., Latreille P., Layman D., Ozersky P., Rohlfing T.,
28 Scheet P., Walker C., Wamsley A., Wohldmann P., Pepin K., Nelson J.,
28 Korf I., Bedell J.A., Hillier L., Mardis E., Waterston R., Wilson R.,
29 Emanuel B.S., Shaikh T., Kurahashi H., Saitta S., Budarf M.L.,
20 McDermid H.E., Johnson A., Wong A.C.C., Morrow B.E., Edelmann L.,
29 Mim U.J., Shizuya H., Simon M.I., Dumanski J.P., Peyrard M., Kedra D.,
20 Seroussi E., Fransson I., Tapia I., Bruder C.E., O'Brien K.P.,
20 Awilkinson P., Bodenteich A., Hartman K., Hu X., Khan A.S., Lane L.,
21 "The DNA sequence of human chromosome 22.";
21 Nature 402:489-495(1999).
  Matches
                    Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         use by non-profit institutions as long modified and this statement is not removed. entitles requires a license agreement (See
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Entropean Bioinformatics Institute. There are no restues by non-profit institutions as long as its content
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                                                                                                                               DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                             Ptam;
                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR000061; Surp.
InterPro; IPR000626; Ubiquitin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Genew;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     or send an email to license@isb-sib.ch).
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                                                                                                         DOMAIN
                                                                                                                                                                                                                                         DOMAIN
                                                                                                                                                                                                                                                                                                                              PROSITE; PS50053;
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                                                                                                                                                                                                                                                             REPEAT
                                                                                                                                                                                                                                                                                      REPEAT
                                                                                                                                                                                                                                                                                                                                                                    PF00240; ubiquitin; PF01805; Surp; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AC004997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            X85237; CAA59494.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HGNC:10765; SF3A1.
67; Conserv
                                                                                                                                                                                                                                                                                                                                                  SM00213; UBQ;
                                                                                  mRNA
52
166
707
10
118
260
369
369
357
672
793
  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAC23435.1;
                                                                                                                                                                                                                                                                                                                          UBIQUITIN_2;
                                                                                                                                                                                                                                                                                                        processing;
                                                                                                                               208
793
16
122
122
372
560
                 7.2%;
                                                                                       WW;
  34;
Score 89; DB
Pred. No. 5.8;
34; Mismatches
                                                                                                                                               UBIQUITIN-LIKE.
POLY-PRO.
POLY-GLN.
POLY-GLU.
POLY-PRO.
                                                                                                                                                                                                                                                           SURP MOTIF 1.
                                                                                                         POLY-PRO
                                                                                                                                  POLY-PRO
                                                                                                                                                                                                                                                                                                     mRNA splicing;
                                                                                       7259F1EC4577305C CRC64,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (See http://www.isb-sib.ch/announce/
                                          μ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Usage by
                                                                                                                                                                                                                                                                                                     Nuclear protein; Repeat.
  79;
                                        Length 793;
  Indels 120;
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4 LAPAWSPTTYLLLLLLLSGLSGTQDCSFQHSPISSDFAVKIRELSDYLLQDYPVTVASN 63

MGD; MGI:104875;

IPR001368;

TNFR\_c6

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 7
                                                                                                                                                                                                                                                                                                    Honjo T.;
Honjo T.;
"The murine lymphotoxin-beta receptor cDNA: isolation by the property of the murine lymphotoxin-beta receptor.";
"Genomics 30:312-319(1995).

Genomics 30:312-319(1995).

-i-FUNCTION: Receptor for the heterotrimeric lymphotoxin containing
-i-FUNCTION: Receptor for TNFS14/LIGHT. Promotes apoptosis via TRAF3

TMA and LTB, and for TNFS14/LIGHT. development of lymphoid organs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Tumor necrosis factor receptor superfamily member
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Browning J.L., Ware
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
STRAIN-CVB; TISSUE-Lung;
MEDLINE-96072804; FubMed-7594541;
Force W.R., Walter B.N., Hession
                            EMBL; U29173; AAA68964.1; -.
EMBL; L38423; AAB00846.1; -.
EMBL; U30798; AAA81334.1; -.
HSSP; O14763; LDOG
                                                                                                            or send an
                                                                                                                                             the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed
                                                                                                                                                                                                               This
                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. MEDLINE=96163885;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LTBR OR TNFRSF3 OR TNFCR.
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                                                                                                                               entities requires
                                                                                                                                                                                                between
                                                                                                                                                                                                                                                                                                                                                                                                                            Nakamura T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Mouse lymphotoxin-beta receptor. Molecular genetics, ligand binding,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (Lymphotoxin-beta receptor).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Immunol.
                                                                                                                                                                                                                                            SUBUNIT: Self-associates (By similarity).
SUBCELLULAR LOCATION: Type I membrane protein.
SIMILARITY: CONTAINS 4 THER-CYS REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            expression
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APQPPLLLLLLPVGLLLLAAAWCLHWQRTR-----RRTPRPGEQVPP---VPSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MPRPPMASVVRLPFGSVIAPMPPIIHAPRINVVPMPPSAPPIMAPRPPPMIVPTAFVPAP 656
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VEETAIGKKIGEEEIQKPEEKVTWDGHSGSMARTQQAAQANIT--LQEQIEAIHKAKGLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VTKCA-----FQPPPSCLRF---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MQEHMRIG-----ILDPRWLEQRDRSIREKQSDDEVYAPGLDIESSLKQLAER-RTDIFG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LQDEELCGGLWRLVLAQRWME-RLKTV------
                                                                                                                                                                                                                                                                                            and TRAF5. May play a role in (By similarity).
                                                                                                                                                                                             SWISS-PROT entry is copyright. It is produced through a collaboration sen the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PEDDTKEKIGPSKFNEIPQQPPPPSSATNIPSSAPPITSVPRPPTMPPPVRTTVVSAVPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ----TRONF--SRCLELQCOP---
                                                                                                              email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            155:5280-5288(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                             Tashiro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                             PubMed=8586432;
                                                                                                                               Latement is not removed. Usage by and for commercial
license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                             K., Nazarea M., Nakano T., Sasayama
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hession C., Tizard R., Kozak C.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -----SPITGE---KI--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -DSSTLP-----PPWSPRPLEAT----APT 180
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                                                                                                                                                            There are no restrictions ong as its content is in
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Best Local
                                                                                                                                                                                                                                                                                                                                  MPIP_DROME STANDARD;
P20483; Q9VAL9;
01-FEB-1991 (Rel. 17, Created)
16-CCT-2001 (Rel. 40, Last sequence upon 15-JUN-2002 (Rel. 41, Last annotation 15-JUN-2002 (Rel. 41, Last annotation
           MEDLINE-91006056; PubMed-2120044; Jimenez J., Alphey L., Nirror
                                                                                                                                                                                         Drosophila melanogaster (Fruit fly).

Bukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

NCBI_TaxID=7227;

[1]
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TRANSMEM
                                                                                                           Edgar B.A., O'Farrell P.H.;
"Genetic control of cell division patterns
   "Complementation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00020; TNFR_c6; 3. ProDom; PD000771; TNFR_c6; 1. SMART; SM00208; TNFR; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  110
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       236
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                                                                                                                                                                                                                                                                                                        OR CDC25 OR CG1395.
                                                                                             57:177-187(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FTTVLACAWMRHPSLCRKLGTLLKRHPE-GEESPPCPAPR 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ----LAAAWCLHWQRTR-----RRTPRPGEQVPPVPSPQ 228
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Alphey L., Nurse ation of fission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7.0%;
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yeast cdc2ts and
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TNFR-CYS 1.
TNFR-CYS 2.
TNFR-CYS 3.
TNFR-CYS 4.
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N-LINKED (GLCNAC. . .) (POTENTIAL)
; 29B326A566AEF661 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 87.5;
Pred. No. 3
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                 Glover D.M
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.48) (String protein) (Cdc25-like
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                                                                                                           in the Drosophila embryo.";
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cdc25ts mutants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1;
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and

for

FlyBase; FBgn0003525; stg.
InterPro; IPR000751; MPI\_Phosphatase.
InterPro; IPR001763; Rhodanese-like.
Pfam; PF00581; Rhodanese: 1

; A32290; A32290. ; S12008; S12008. ;P; P30304; 1C25.

M24909; AAA28916.1; -. X57495; CAA40732.1; -. AE003768; AAF56885.1;

PRINTS;

PR00716;

MPIPHPHTASE

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RA Ballew R.M. Basu A. Baxendale J. Bayraktaroglu L. Beasley E.M.,
RA Beeson K.Y. Benos P.V. Berman B.P. Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Borkova D., Butler H., Cadieu E., Center A., Chandra I.,
RA Borkova D., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Borkova D., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Dorson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Gelbart W.M., Glasser K.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Melson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Zheng X.H., Woodage T., Worley K.C., Wu D. S., Zhu X., Smith H.O.,
RA Shin B. S., Shore
the European Bioinformatics Institute. There are no rest use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an
                                                                                                                                                                                                                                                                                                                             George R.A., Lewis S.E., Richards S., Ashburner M., Henderson Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwani J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwani A., An
                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  identifies two cell cycle genes from Drosophila: a cdc2 homologue and string."; EMBO J. 9:3565-3571(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=20196006;
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Smith H.O.,
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                                                                                                                                                                      DDR1_RAT STANDARD; PRT; Y1U AA.

Q63474;
Q63474;
Q1-NOV-1997 (Rel. 35, Created)
Q1-NOV-1997 (Rel. 35, Last sequence update)
Q1-NOV-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
Epithelial discoidin domain receptor 1 precursor (EC 2.7.1.112)
Epithelial discoidin kinase CAK) (Cell adhesion kinase) (Tyrosine kinase
(Tyrosine-protein kinase CAK) (Cell adhesion kinase) (Tyrosine kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sanchez M.P., Tapley P., Saini S.S., He B., Pulido D., Barbaci "Multiple tyrosine protein kinases in rat hippocampal neurons: isolation of Ptk-3, a receptor expressed in proliferative zone
                                             This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-Sprague-Dawley; TISSUE-Brain; MEDLINE-94173920; PubMed-8127887;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=10116;
[1]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rattus norvegicus (Rat).
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                         between
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SIMILARITY:
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                                                                                         RECEPTOR SUBFAMILY.
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                         SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation -
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    Bioinformatics
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BELONGS TO
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Rodentia;
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                                                                                                                                                                             TYON: Type I membrane protein.
TY: VARIOUS EMBRYONIC AND ADULT TISSUES; ALSO
NES OF THE DEVELOPING BRAIN; HIPPOCAMPAL NEURONS
THE CONSERVED CATALYTIC DOMAINS OF TYR-PROTEIN
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Pred.
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                                                                                                             '8 TYPE C DOM
TYR FAMILY
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                                                                                                                PROTEIN
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; Murinae; Rattus
                                                                                                                KINASES.
  restrictions
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RESULT 10
DDR1\_MOUSE
ID DDR1\_M
AC Q03146
DT 01-OCT
DT 01-VOV
DT 15-JUN
DE Epithe
DE (Tyros

Q03146;

DDR1\_MOUSE

STANDARD;

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003445; 01-OCT-1994 (Rel. 30, Created) 01-NOV-1997 (Rel. 35, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update) Epithelial discoidin domain receptor 1 precursor (EC

kinase

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Best Local S
Matches 38
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CARBOHYD
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DOMAIN
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SMART; SM00219; TyrK; 1.
SMART; SM00219; TyrK; 1.
SPROSITE; SE00109; PROTEIN_KINASE_TYR; 1.
PROSITE; PS00239; RECEPTOR_TYR_KIN_II;
PROSITE; PS01285; FA58C_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00069; pkinase; 1. Pfam; PF00754; F5_F8_type_C; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ProDom; PD000001; Euk_pkinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HSSP; P00523; 2PTK
                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                  CARBOHYD
                                                                                                                                                                                                                                                                                                                                                      CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DISULFID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Transterase;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS01286;
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                                                                                                                                                                                                                                                                                                                                                                                                                MOD_RES
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471
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                                                                                                                                                                             PWITRQNFSRCLELQCQPDSSTLPP-PW----SPRPLEATA----PTAPQP----
NRPGPREPPPYQEPRPRGTPTHSAPCVPNGSALLL
                                   PRPGEQVPP
                                                                                                                                                      PWLLFSEISFISDV-VNDSSDTFPPAPWWPPGPPPTNFSSLELEPRGQQPVAKAEGSPTA 414
                                                                            ILIGCLVAIILLLLIIALML---
                                                                                                                                                                                                                                   . Similarity
38; Conser
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                                                                                                                 --PLLLLLLEPVGLLLLAAAWCLHWQR----TRRR---
                                                                                                                                                                                                                                                                                                                 910
                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0011; PROTEIN_KINASE_DOM; 1.
Tyrosine-protein kinase; Glycoprotein; S
ion; Transmembrane; Receptor; ATP-binding
                                                                                                                                                                                                                                                                                                       18 412

3 598

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24.5%;
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N-LINKED
N-LINKED
                                                                                                                                                                                                                                                       Score 87;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                              PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
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ATP
BY S
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F5/8 TYPE C
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                                                                            -WRLHWRRLLSKAERRVLEEELTVHLSVPGDTILIN
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                                     -VPSPQDLLL
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SIMILARITY
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SIMILARITY).
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(GLCNAC...)
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                                                                                                                                                                                                                                                       DB
10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (POTENTIAL)
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PROSITE;

PROSITE;

Transferase; ...

Phosphorylation; 'L...

Phosphorylation; 'L...

Phosphorylation; 'L...

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20

911
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PROSITE; |
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PROSITE; |
PROSITE; |
PROSITE; |
                                                                                                                                                                                                Interro.

Pfam; PF00069; pkinase; 1.

Pfam; PF00754; F5_F8_type_C; 1.

PF00000001; Euk_pkinase;
                                                                                                                                                                              SMART;
                                                                                                                                                                                                                                                                                                                                                                                    use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                              MGD; MGI:99216; Ddrl.
InterPro; IPR000719; Euk_pkinase.
InterPro; IPR000421; FA58_C.
InterPro; IPR002011; RTKinaseII.
InterPro; IPR001245; Tyr_pkinase.
                                                                                                                                                                                                                                                                                                                                  EMBL; L57509; AAB05209.1;
EMBL; X57240; CAA40516.1;
PIR; S30502; S30502.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gilardi-Hebenstreit P., Nieto M.A., Frain M., Mattei M.-G., Chestler A., Wilkinson D.G., Charnay P.;
"An Eph-related receptor protein tyrosine kinase gene segmentally expressed in the developing mouse hindbrain.";
Oncogene 7:2499-2506(1992).
-!- FUNCTION: MAY BE INVOLVED IN CELL-CELL INTERACTIONS AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Oncogene
                                                                                                                                                                                                                                                                                                                       HSSP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Perez J.L., Jing S.Q., Wong T.W.; "Identification of two isoforms of the Cak receptor kinase that coexpressed in breast tumor cell lines."; Oncogene 12:1469-1477(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   <del>-</del>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=C57BL/6; TISSUE=Embryonic MEDLINE=93096484; PubMed=1281307;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 766-822 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=96204002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=C57BL/6;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mammalia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MPK-6)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 tyrosine phosphate.

SUBCELLULAR LOCATION: Type I membrane protein.

LALTERNATIVE PRODUCTS: 2 ISOFORMS; CAK I (SHOWN ARE PRODUCED BY ALTERNATIVE SPLICING. THEY ONLY ABSENCE OF A 37 RESIDUES SEGMENT.

TISSUE SPECIFICITY: THE PREDOMINANT ISOFORM CAK DEVELOPING EMBRYO AND ADULT BRAIN; CAK II IS EXECUTED IN CELLS.

SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                   European Bioinformatics Institute. The by non-profit institutions as long
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RECEPTOR SUBFAMILY.
SIMILARITY: CONTAINS 1 F5/8 TYPE C DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CATALYTIC ACTIVITY: ATP + a protein tyrosine =
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RECOGNITION (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                           SWISS-PROT entry is copyright. It is produced through a collaboration en the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OR EDDR1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (Discoidin
                                                                                                                SM00231; FASEC; 1.

SM00231; FASEC; 1.

SM00239; TYPKC; 1.

PE; PS00107; PROTEIN KINASE_ATP; FAL:

PE; PS00109; PROTEIN_KINASE_TYR; 1.

PE; PS0011; PROTEIN_KINASE_DOM; 1.

PROTEIN_KINASE_TYR_KIN_II; 1.
                                                                                                                                                                                                                                                                                                                       P00523; 2PTK.
                                                                                           PS01285; FA58C_1; PS01286; FA58C_2;
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                                                                           Tyrosine-protein kinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (Mouse)
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                                                            Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PubMed=8622863;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chordata;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      tyrosine
       EPITHELIAL DISCOIDIN DOMAIN RECEPTOR EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Craniata; Ver
Sciurognathi;
                                                               Receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   kinase) (Protein-tyrosine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SPLICING
                                                            Glycoprotein; Si
tor; ATP-binding;
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                                                                                                                                                                                                                                                                                                                                                                                                                            There are no rest
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thi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        protein.
I (SHOWN HERE)
THEY ONLY DIFFE
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S EXPRESSED
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                                                                           Signal;
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; Murinae; Mus
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PRESENTATION OF THE PRESEN
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CNG4_BOVIN
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       CNG4_BOVIN STANDARD; PRT; 1394 AA.

Q28181; Q28082; Q03861;

Q1-NOV-1997 (Rel. 35, Created)

Q1-NOV-1997 (Rel. 35, Last sequence update)

Q1-NOV-1997 (Rel. 40, Last annotation update)

16-OCT-2001 (Rel. 40, Last annotation complete)

240 kDa protein of rod photoreceptor CNG-channel (Contains: Glutamic acid-rich protein (GARP); Cyclic-nucleotide-gated cation channel 4

(CNG channel 4) (CNG-4) (Cyclic nucleotide-gated cation channel modulatory subunit)].
                                                                                                                                                                                                                    SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
MEDLINS-96009859; pubMed-7546742;
MEDLINS-96009859; pubMed-7546742;
Koerschen H.G., Illing M., Seifert R., Sesti F., Williams A.,
Gotzes S., Colville C., Mueller F., Dose A., Godde M., Molday L.,
Kaupp U.B., Molday R.S.;
                                     MEDLINE=96198098; PubMed=8626431;
Biel M., Zong X., Ludwig A., Sautter A.,
"Molecular cloning and expression of the
                                                                                                                                                             Kaupp U.B., Molday R.S.;
"A 240 kba protein represents the nucleotide-gated channel from rod Neuron 15:627-636(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOD_RES
cyclic nucleotide-gated cation channel.";
J. Biol. Chem. 271:6349-6355(1996).
                                                                             TISSUE=Testis;
MEDLINE=96198098;
                                                                                                                                                                                                                                                                                                                                                                Mammalia; Eutheria
Bovidae; Bovinae;
                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                CNGB1 OR CNCG4.
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ACT_SITE
                                                                                                                     SEQUENCE OF 454-1394 FROM N.A.
                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=9913;
                                                                                                                                                                                                                                                                                                                                                                                                                           Bos taurus (Bovine).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              143 PWITRQNFSRCLELQCQPDSSTLPP-PW---SPRPLEATA----PTAPQP------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local
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186
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N-LINKED (GLCNAC. . .)
N-LINKED (GLCNAC. . .)
N-LINKED (GLCNAC. . .)
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PHOSPHORYLATION
PHOSPHORYLATION
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Pred. No.
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PROTEIN KINASE
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BY SIMILARITY
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ATP (BY SIMILARITY).
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POTENTIAL).
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                                                                                                                                                                        photoreceptor.";
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                                     modulatory subunit of
                                                        Hofmann
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(AUTO-)
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PROSITE; PS00889; CNMP_BINDING_2; 1.
PROSITE; PS50042; CNMP_BINDING_3; 1.
Ionic channel; Ion transport; CAMP-b.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collabora between the Swiss Institute of Bioinformatics and the EMBL outstatithe European Bioinformatics Institute. There are no restrictions on use by non-profit institutions as long as its content is in no modified and this statement is not removed. Usage by and for commen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00027; cNMP_binding; 1.
Pfam; PF00520; ion_trans; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -i- SUBCELLULAR LOCATION: Integral membrane protein.
-i- ALTERNATIVE PRODUCTS: 3 ISOFORMS; CNG4C (SHOWN HERE), CNG4D
-i- ALTERNATIVE PRODUCED BY ALTERNATIVE SPLICING. CNG4D IS BY FAR
AND CNG4E; ARE PRODUCED BY ALTERNATIVE SPLICING. CNG4D IS BY FAR
THE MOST PREQUENT FORM (CNG4D:CNG4C:CNG4E = 20:2:1) IN TESTIS.
-i- TISSUE SPECIFICITY: RETINA, TESTIS, KIDNEY, HEART, AND BRAIN.
-i- SIMILARITY: BELONGS TO THE CYCLIC NUCLEOTIDE-GATED CATION CHANNEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sugimoto Y., Yatsunami K., Tsujimoto M., Khorana H.G., Submitted (XXX-1991) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                              CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR000636; M+channel_nlg
InterPro; IPR000595; cNMP_binding.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -!- SUBUNIT: FORMS FUNCTIONAL HETEROOLIGOMERIC CHANNELS WITH CNG3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE=Retina;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 1-590 FROM N.A.
  115 PPPSCLRFVQTNISRLL--
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X94707; CAA64367.1; -.
M61185; AAA30536.1; -.
                                           35; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       email to license@isb-sib.ch).
                                                                                                                                                                                                                                                     768
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24.6%;
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S -> A (IN REF.
R -> A (IN REF.
D -> E (IN REF.
A -> AA (IN REF.
                                                                                                                           WW;
                                         Score 86.5; DI
Pred. No. 18;
L3; Mismatches
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GLUTAMIC ACID-RICH PROTEIN.
CYCLIC-NUCLEOTIDE-GATED CATION CHANNEL
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                                                                                                                                                                                                                                                                                                                                                      N-LINKED (GLCNAC. . .) (POT MISSING (IN ISOFORM CNG4E). MISSING (IN ISOFORM CNG4D).
                                                                                                                                                                                                                                                                                                                                                                                                                     CAMP (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                         CAMP (BY SIMILARITY).

CAMP (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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                                                                                                                           EE6DA559BE3744A7 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (POTENTIAL).
-QETSEQLVALKPWITRQNFSRCL 154
                                                                                  DВ
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                                           53;
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                                                                                  Length 1394;
                                           Indels
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01-AUG-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for competities requires a license agreement (con the content is in the content is a content in the content is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Glycoprotein; su 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the cellular compartment.";

J. Cell Biol. 109:3493-3501(1989).

-i- FUNCTION: THE EXTRACELLULAR MATRIX (ECM) OF VOLVOX CONTAINS INSOLUBLE FIBRCUS LAYERS THAT SURROUND INDIVIDUAL CELLS AT A DISTANCE TO FORM CONTIGUOUS CELLULAR COMPARTMENTS. SSG 185 IS MONOMERIC PRECURSOR OF THIS SUBSTRUCTURE (C3Z STRUCTURE). THE CONALENT CROSS-LINKS ARE FORMED BETWEEN THE SACCHARIDE CHAINS RATHER THAN BETWEEN THE POLYDEDTIDE CHAINS.

-i- PTM: A CENTRAL DOMAIN OF 77 AA CONSISTS ALMOST EXCLUSIVELY OF HYDROXYEROLINE RESIDUES.
ATF5_HUMAN
Q9Y2D1; Q9U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PIR; A33647; A33647. Glycoprotein; Sulfation; Hydroxylation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-OCT-1996 (Rel. 34, Last annotation update) surface glycoprotein 185 (SSG 185).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-AUG-1991 (Rel. 19, Created)
01-AUG-1991 (Rel. 19, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A., AND PARTIAL SEQUENCE STRAIN=f. Nagariensis / HK10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Volvox carteri
Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; X51616; CAA35953.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ertl H., Mengele R., Wenzl S., Engel J., Sumper M.;
"The extracellular matrix of Volvox carteri: molecular structure
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=90094551; PubMed=2689458;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Volvocaceae; Volvox.
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                                                                                                                                                                                                                                                                                                                                               160 PDSSTLPPPWSPRFLEATAPTAPQPPLLLLLLPVGLLLLAAAWCLHWQRTRRRTPRPGE 219
                                                                                                                                                                            PVPPPPSPPSVL 320
                                                                                                                                                                                                                               QVPPVPSPQDLL
                                                                                                                                                                                                                                                                                           PRP----GEQVPPVPSPQDL 230
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   Q9UNQ3;
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485 AA;
                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                           STANDARD;
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295
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                                                                                                                                                                                                                                                                                                                                                                                                                                   6.9%;
                                                                                                                                                                                                                                                                                                                                                                                                        score 86; DB 1; Pred. No. 5.9; 3; Mismatches
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SOLUTION OF THE STREET OF THE 
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Best Local S
Matches 38
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AF305687; AAG22558.1; -.
EMBL; AB02163; BAA78477.2; -.
EMBL; AF101388; AAD28370.1; -.
TRANSFAC; T04877; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 White J.H., McIllhinney R.A.J., Wise A., Ciruela F., Chan W.Y., Emson P.C., Billinton A., Marshall F.H.; "The GABAB receptor interacts directly with the related transcription factors CREB2 and ATFx.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens (Human).
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16-OCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Cyclic-AMP-dependent transcription factor ATF-5 (Actional Control of the Control 
                                                                                                                                                                                                                                                                                                                                                                                    CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Genew; HGNC:790; ATF5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pati D., Meistrich M.L., Plon S.E.; "Human CdC34 and Rad6B ubiquitin conjugating enzymes target repressors of cyclic AMP-induced transcription for proteolysis."; Mol. Cell. Biol. 19:5001-5013(1999).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Multigene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATF5 OR ATFX.
       179
                                                                                                                                      144
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FUNCTION: THIS PROTEIN BINDS THE CAMP RESPONSE (CONSENSUS: 5'GTGACGT(A/C)(A/G)-3'), A SEQUENCE VIRAL AND CELLULAR PROMOTERS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUBCELLULAR LOCATION: Nuclear (By similarity). SIMILARITY: BELONGS TO THE BZIP FAMILY.
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                                                                                                                                   WIT-RQNESRCLELQCQPDSSTLPPPWSPRP--LEATA-----
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       ---PTAPQPPLLLLLLPVGL
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                                                               WMTERVDFTALLPLEPPLPPGTLPQP-SPTPPDLEAMASLLKKELEQMEDFFLDAPPLPP 124
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                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PS00036; BZIP_BASIC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ., Tanaka K.; (DEC-1998) t
                                                                                                                                                                                                                                                                                                                                             161
282 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                 123
186
210
236
                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    regulation;
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                                                                                                                                                                                                                                                                                                                                                                                 139
194
230
250
163
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                                                                                                                                                                                                                                                                                                                                                 30674 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA-binding; Activator;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                      Score 85;
Pred. No.
                                                                                                                                                                                                      Pred. No. 3.9;
7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                          LEUCINE-ZIPPER
                                                                                                                                                                                                                                                                                                                                                                                                                                             BASIC MOTIF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    POLY-PRO
                                                                                                                                                                                                                                                                                                                                             DDB2F907CA0215A0 CRC64;
-LLLAAAWCLH--WQRTRRRTPRPGEQ
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                                                                                                                                                                                                                                                                                                                                                                                 REF
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                                                                                                                                                                                                                                                                                                                                                                                                          (PROBABLE).
                                                                                                                                                                                                                                                                      Length
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                                                                                                                                                                                                          Indels
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LRAT
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    entities requires a license agreement or send an email to license@isb-sib.ch
                                                                                                                                                                                                                                                                                      Structure 6:63-73(1998).

-!- FUNCTION: BINDS TO THE FC REGION OF MONOMERIC IMMUNOGLOBULINS GAMMA. MEDIATES THE SELECTIVE UPTAKE OF IGG FROM MILK AND HELPS NEWBORN ANIMALS TO ACQUIRE PASSIVE IMMUNITY. IGG IN THE MILK IS BOUND AT THE APICAL SURFACE OF THE INTESTINAL EPITHELIUM. THE RESULTANT FORN-IGG COMPLEXES ARE TRANSCYTOSED ACROSS THE INTESTINAL EPITHELIUM AND IGG IS RELEASED FROM FCRN INTO BLOOD CONSIST OF TWO SUBUNITS: P51, AND P14 WHIGH SUBUNITS: FCRN COMPLEX CONSIST OF TWO SUBUNITS: P51, AND P14 WHIGH SUBUNITS: P51, AND P14 WH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=95059482; PubMed=7969498;
Burmeister W.P., Huber A.H., Bjorkman P.J.
"Crystal structure of the complex of rat r
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Simister N.E., Mostov K.E., 
"Cloning and expression of the meonatal rat intestinal Fc 
major histocompatibility complex class I antigen homolog." 
Cold Spring Harb. Symp. Quant. Biol. 54:571-580(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JAN-1990 (Rel.
15-JUN-2002 (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Crystal structure Fc.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FCGRT OR FCRN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IGG receptor FCRN receptor) (IGG FC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Vaughn D.E., Bjorkman P.
"Structural basis of pH-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nature 372:379-383(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=90315866; PubMed=2534798;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE=Epithelium;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "An Fc receptor structurally related Nature 337:184-187(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Simister N.E., Mostov K.E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=89097257; PubMed=2911353;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=10116;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JAN-1990
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          185
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                                                                                                                                                                                             SUBCELLULAR LOCATION: Type I membrane protein. TISSUE SPECIFICITY: INTESTINAL EPITHELIUM. SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.
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                                                                                                                                                                                                                                                                       HETERODIMER.
                   email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                large subunit P51 fragment receptor

    Last sequence update)
    Last annotation update)

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Best Local
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CARBOHYD
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CARBOHYD
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DOMAIN
                                    SEQUENCE FROM N.A.
STRAIN-BALB/MK X ICR; TISSUE-Brain;
MEDLINE-96194902; PubMed-8654949;
MEDLINE-96194902; Tartenaha M. Saka
                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia;
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DOMAIN
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SIGNAL
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SMART; SM00407; IGc1; 1.
PROSITE; PS00290; IG_MHC; 1
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InterPro; IPR003597; Ig_c1.
InterPro; IPR001039; MHC_I.
     Hashimoto
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                            A., Miura Y.,
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A37374;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RELSDYLLQDYPVTVASNLQDEELCGGLWRLVLAQRWME----RLKTVAGSKMQGLLERV
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3FRU; 10-JUN-98
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M35495; AAA41611.1;
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51; Conservative
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22.2%;
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M., Sakai
Nishi S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -QCQPDSSTLPPPWSPRPLEATAPTAPQPPLLLLLLLPVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21;
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CYTOPLASMIC (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

BY SIMILARITY.

BY SIMILARITY.

N-LINKED (GLUNAC...) (POUR N-LINKED (GLUNAC...)) (POUR N-LINKED (GLUNAC...) (POUR N-LINKED (GLUNAC...)) (POUR N-LINKED (GLUNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 85; DB
Pred. No. 5.2;
21; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-LINKED (GLCNAC. ..) (PO N-LINKED (GLCNAC. ..) (PO N-LINKED (GLCNAC. ..) (PO N-LINKED (GLCNAC. ..) (PO BA8BF2873A698BB5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EXTRACELLULAR ALPHA-2.
EXTRACELLULAR ALPHA-3.
                                                                                                                                                                             Craniata; Ver
Sciurognathi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EXTRACELLULAR ALPHA-1
                            Sakai
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  M., Inou
                                                                                                                                                                          Vertebrata;
thi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 1;
5.2;
     Inoue
aoki T.
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SMART; SM00355; Znf_C2H2; 22.
SMART; SM00451; Znf_U1; 7.
PROSITE; PS00027; HOMEOBOX_1;
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InterPro; IPR001356; Homeobox.
InterPro; IPR000822; znf_C2H2.
InterPro; IPR003604; znf_U1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- FUNCTION: Transcriptional activator sequence of the enhancer element of SUBCELLULAR LOCATION: Nuclear.
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Search completed: November 24, 2002, 10:10:39 Job time : 12.573 secs	Qy 224 VPSPQ 228 : :   Db 3225 IPAPQ 3229	QY 171 PRPLEATAPTAPQPPLLLLLLLPVGLLLLAAAWCLHWQRTRRRTPRPGEQVPP	QY 127 ISRLIQETSEQLVALKPWITRQNFSRCLELQCQPDSSTLPPPWS	Qy 87 KTVAGSKMQGLLERVNTEIHFVTKCAFQPPPSCLREVQTN 126	QY 29 DCSFQHSPISSDFAVKIRELSDYLLQDYPYTVASNLQDEELCGGLWRLYLAQRWMERL	372	FT DOMAIN 3620 3623 POLY-PRO. FT DOMAIN 3659 3662 POLY-SER. SQ SEQUENCE 3726 AA; 406567 MW; 915ACBE588A72C98 CRC64;
		LHWQRTRRRTPRPGEQVPP 223PQPQQPQPPVQQPPPPPAAQQ 3224	PPPW	-PPPSCLREVQTN 126 	ELCGGLWRLVLAQRWMERL 86 :   ::  : :: : KEYFDPATVRQLMAQQELDRI 3092	1; Length 3726; 70; Indels 93; Gaps 12;	72098 CRC64;

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Q99mml mus musculu Q9p2d0 homo sapien	Q9a3k1 caulobacter		Q95uq2 toxoplasma	O35407 mus musculu	Q23600 caenorhabdi	Q84647 paramecium	Q9d3j3 mus musculu	Q9ttt9 bos taurus	Q8ta74 hemicentrot	O44018 leishmania	O22015 cylindrothe	Q9luil arabidopsis	056971 kennedya ye		Q9gke2 sus scrofa	075064 homo sapien	Q943d5 oryza sativ	Q9awj4 oryza sativ	Q9umt1 homo sapien	Q8ywx3 anabaena sp	017610 caenorhabdi	Q9pu36 gallus gall	Q9gy15 leishmania		Q9had2 homo sapien	Q8szs7 drosophila	Q9gyal leishmania

## ALIGNMENTS

Qy	DЬ	Qy	Db	Qу	<b>X</b> B <b>X</b>	)	SQ	DR	DR	DR	RL	RT	RT	RT	RA	RX	RP	RN	o <b>x</b>	8	8	SO	DE	DT	DT	DT	AC	ID Q	RESULT
121 RFVQTNISRLLQETSEQLVALKBWITRONFSRCLELQCQPDSSTLPPPWSPRPLEATAPT 180	61 ASNLQDDELCGAFWRLVLAQRWMVRLQAVAGSQMQILLEAVNTEIHFVTFCAFQPLPSCL 120	61 ASNIQDEELCGGLWRLVLAQRWMERLKTVAGSKMQGLLERVNTEIHFVTKCAFQPPPSCL 120	1 MIVLAPAWSPTASLLLLLLLLSPGLRGTPDCSFSHSPISSTFAVTIRKLSDYLLQDYPVTV 60	1 MTVLAPAWSPTTYLLLLLLLSSGLSGTQDCSFQHSPISSDFAVKIRELSDYLLQDYPVTV 60	Best Local Similarity 77.1%; pred. No. 3.5e-80; mest Local Similarity 77.1%; pred. No. 3.5e-80; mest Local Similarity 77.6aps 3; Matches 182; Conservative 12; Mismatches 35; Indels 7; Gaps 3;	72 14. 8000 805 5. 15 6.	SEQUENCE 294 AA; 32394 MW; 6859917A3B74ABCD CRC64;	Pfam; PF02947; flt3_lig; 1.	InterPro; IPR004213; Flt3_lig.	EMBL; AF155148; AAF87088.1;	DNA Seq. 11:163-166(2000).	long cytoplasmic domain.";	n and mouse homologue but w	"Molecular cloning of canine and feline flt3 ligand reveals high	Yang S., Sim G.K.;	MEDLINE=20358731; PubMed=10902925;	SEQUENCE FROM N.A.	[1]	NCBI_TaxID=9615;		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	Canis familiaris (Dog).	•	(TrEMBLrel. 21, Last	15,	-2000 (TrEMBLrel.	••	Q9M2V0 PRELIMINARY; PRT; 294 AA.	ULT 1

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Sim
Matches 178;
                                                                                                                                                                                                                                                                  Q9GKE0;
Q1-MAR-2001 (TrEMBLrel. 16, C
Q1-MAR-2001 (TrEMBLrel. 16, I
Q1-DEC-2001 (TrEMBLrel. 19, I
F1L3 ligand isoform-1.
                                                                                                                                                  Mammalia; Butheria; Cetartiodactyla; Ruminantia; Bovidae; Bovinae; Bos. NCBI_TaxID=9913;
                    SEQUENCE FROM N.A.

MEDLINE=20570936; PubMed=11120823;

MWANDI W. Brown W.C., Palmer G.H.;

"Identification of fetal liver tyrosine kinase 3 (Flt3) ligand domain

"required for receptor binding and function using naturally occurring
                                                                                                                                                                                                                           Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata;
                                                                                                                                                                                                                                                                                                                                                                                           Q9GKE0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Yang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Felis silvestris catus (Cat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Carnivora; Fissipedia; Felidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-OCT-2000 (TrEMBLrel. 15, 01-OCT-2000 (TrEMBLrel. 15, 01-JUN-2002 (TrEMBLrel. 21,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA Seq. 11:163-166(2000).
EMBL; AF155149; AAR87089.1, -.
InterPro; IPR004213; Flt3_lig.
Pfam; PF02947; flt3_lig; 1.
SEQUENCE 291 AA; 32459 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 degree of similarity to the long cytoplasmic domain.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Flt3 ligand.
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01-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=20358731; PubMed=10902925;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=9685;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q9MZU9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Н
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APQPP-LLLLLLLPVGLLLLLAAAWCLHWQRTRRRTPRPFGEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RFVQTNISRLLQETSEQLVALKPWITRQNFSRCLELQCQPDSSTLPPPWSPRPLEATAPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  S., Sim G.K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APQAPLILLLLPVALLLMSAAWCLHWRRRRWRTPYPREQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ASNLQDEELCGGLWRLVLAQRWMERLKTVAGSKMQGLLERVNTEIHFVTKCAFQPPPSCL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RFVQTNISHLLQDTSEQLAALKPWITRRNFSGCLELQCQPDSSTPLPPRSPRALEATALP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APQPP-LLLLLLPVGLLLLAAAWCLHW-QRTRRRTPRPGEQVPPVPS-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ASNLQDDELCGPFWHLVLAQRWMGRLKAVAGSQMQSLLEAVNTEIHFVTLCAFQPLPSCL
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      isoforms
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Last sequence update)
Last annotation updat
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Last annotation updat
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Pred. No. 4.3e-80;
9; Mismatches 33;
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                                                                                                                                                                                                                           Vertebrata;
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Best Local
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Best Local
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Q1-MAR-2002 (TrEMBLrel. 2

Q1-MAR-2002 (TrEMBLrel. 2

Q1-JUN-2002 (TrEMBLrel. 2

Flt3 ligand.

FLT3 LIGAND.
                                                                                                                                                                                                                                                            Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases. EMBL; AB051841; BAB79634.1; -. InterPro; IDFR004213; Flt3_lig. Pfam; PF02947; Flt3_lig; 1. SEQUENCE 292 AA; 32388 MW; 2A797E0C1199C1D9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                      Bos taurus (Bovine).
Eukaryota; Metazoa: Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea
Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     J. Immunol. 165:6966-6974(2000).
EMBL, AF283985; AAF99322.1; -.
InterPro; IPR004213; F1t3_lig.
Pfam; PF02947; f1t3_lig; 1.
SEQUENCE 292 AA; 32390 MW; D
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                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=9913;
                                                                                                                                                                                                                                                                                                                            Hikono H., Momotani E.;
"Cloning of a cDNA for bovine
                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
181
                         180
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PGPQSPLLLLLLLLLPVALLLLATAWCLCRWRRRRRTRYPGER
                        TAPQPP----LLLLLLPVGLLLLAAAWCLHWQRTRRRTPRPGEQ 220
                                                              LREVQTNISRLLQETSEQLVALKPWITRQNESRCLELQCQPDSSTLPPPWSPRPLEATAP
                                                                                                    VASNLQDDKLCGAFWRLVLAQRWMGRLKTVAGSEMEKLLEDVNTEIHFVTSCAFQPLPSC
                                                                                                                  VASNLQDEELCGGLWRLVLAQRWMERLKTVAGSKMQGLLERVNTEIHFVTKCAFQPPPSC
                                                                                                                                                     MTVLAPAWSPTT-YLLLLLLLSSGLSGTQDCSFQHSPISSDFAVKIRELSDYLLQDYPVT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LREVQTNISRLLQETSEQLVALKPWITRQNFSRCLELQCQPDSSTLPPPWSPRPLEATAP 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VASNLQDEELCGGLWRLVLAQRWMERLKTVAGSKMQGLLERVNTEIHFVTKCAFQPPPSC
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                                                LRFVQANISHLLQDTHQQLEALKPWITHRNFSRCLELQCQPDSPTLLPPRSPGALGATSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VASNLQDDKLCGAFWRLVLAQRWMGRLKTVAGSEMEKLLEDVNTEIHFVTSCAFQPLPSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               {\tt MTVLAPAWSPTTSLLLLLLLSPGLQGTPDCSFRHSPISSTFAIKIGKLSKYLLQDYPVT}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LRFVQANISHLLQOTHQQLEALKPWITHRNFSRCLELQCQPDSPTLLPPRSPGALGATSL
                                                                                                                                                                                                           170;
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                                                                                                                                                                                                                         Similarity
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75.9%;
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76.3%;
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20,
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Last annotation update)
                                                                                                                                                                                                        Score 835; DB 6;
Pred. No. 3.2e-74;
2; Mismatches 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Created)
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                                                                                                                                                                                                                                                                                                                            flt3 ligand."
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Best Local
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                forms and processing.";
submitted (DEC-1995) to the EMBL/Ge
EMBL; U44024; AAA93305.1; -.
MGD; MGI:95560; F1131.
InterPor: IPR004213; F1t3_lig.
InterPor: IPR001230; Prenyl_site.
Pfam; PF02947; f1t3_lig: 1.
                                                                                                                                   SEQUENCE FROM N.A.

McClanahan T., Culpepper J.

Mattson J., Tsai S., Luh J.

Birnbaum D., Hannum C.;

"Flt3 ligand: expression, grant gra
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-MAR-2001
01-DEC-2001
Flt3 ligand
                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1996
01-NOV-1996
01-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q9GKD9;
01-MAR-2001
                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q61104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bos taurus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q9GKD9
                                                                                                                                                                                                                                                                                                                                   Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR004213; Flt3_lig. Pfam; PF02947; flt3_lig; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=20570936; PubMed=11120823;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=9913;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bovidae; Bovinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               163
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Immunol. 165:6966-6974(2000).
                                                                                                                                                                                                                                                                                                                                                                          ligand,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PGPQSPLLLLLLLLFVALLLLATAWCLCRWRRRRTRYPGER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LRFVQTNISRLLQETSEQLVALKPWITRQNFSRCLELQCQPDSSTLPPPWSPRPLEATAP 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VASNLQDEELCGGLWRLVLAQRWMERLKTVAGSKMQGLLERVNTEIHFVTKCAFQPPPSC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VASNLQDDKLCGAFWRLVLAQRWMGRLKTVAGSEMEKLLEDVNTEIHFVTSCAF-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MTVLAPAWSPTTSLLLLLLLLSPGLQGTPDCSFRHSPISSTFAIKIGKLSKYLLQDYPVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              156;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
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1 (TrEMBLrel.
1 isoform-2.
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                                                                                                                                                                                                                                                                                                                                                                            (TrEMBLrel.
(TrEMBLrel.
1, T169 form.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QDTHQQLEALKPWITHRNFSRCLELQCQPDSPTLLPPRSPGALGATSL
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PRENYLATION; UNKNOWN_1
                                                                                                                                                                                                                                                                                                Chordata;
Rodentia;
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19,
                                                                                                                                                                                           genomic
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                                                                                                                     EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                     Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 746; DB 6; Pred. No. 1.8e-65;
                                                                                                                                                                                           Campbell D., W. Guimares M.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                           Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            725A7F77A95DA98B
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                                                                                                                                                        organization,
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                                                                                                                                                                                             Wagner J., Fra
., Mattei M.-G.
                                                                                                                                                                                                                                                                                                                                                                                                update)
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                                                                                                                                                                                                                 Franz-Bacon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   274;
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                                                                                                                                                                                               Rosnet
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RESULT
Q8VCH4
ID Q8
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Q9LGG8
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Best Local S
Matches 120
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                                           Q9LGG8;
Q9LGG8;
Q1-OCT-2000 (TrEMBLrel. 15, Created)
Q1-OCT-2000 (TrEMBLrel. 15, Last sequence up
Q1-JUN-2002 (TrEMBLrel. 21, Last annotation
Putative extensin-like protein.
P0406H10.6 OR QJ1174_D05.5.
Qryza sativa (Rice).
                                                                                                                                                                                                                                                                                                                                                                                                                   Summitted (DEC-2001) to the EMBL/GenBank/DDBJ EMBL; BC019801; AAH19801.1; -. Interpro; IPR004213; Flt3_lig. Pfam; PF02947; flt3_lig; 1. Kinse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  08VCH4;
01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Similar to FMS-like tyrosine kinase 3 ligand.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Trach Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
NCBI_TaxID=4530;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus (Mouse)
                                                                                                                                      Q9LGG8
                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Strausberg R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE-LIVER;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                  VAVNLQDEKHCKALWSLFLAQRWIEQLKTVAGSKMQTLLEDVNTEIHFVTSCTFQPLPEC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LREVQTNISHLLKDTCTQLLALKPCIGKACQNFSRCLEVQCQPDRVSL
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                                                                                                                                                                                                                LRFVQTNISRLLQETSEQLVALKPWITR--QNFSRCLELQCQPDSSTLPPPWSPR
                                                                                                                                                                                                                                                                                                              MTVLAPAWSP-TTYLLLLLLLSSGLSGTQDCSFQHSPISSDFAVKIRELSDYLLQDYPVT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VASNLQDEELCGGLWRLVLAQRWMERLKTVAGSKMQGLLERVNTEIHFVTKCAFQPPPSC
                                                                                                                                                                                                   LRFVQTNISHLLKDTCTQLLALKPCIGKACQNFSRCLE-----
                                                                                                                                                                                                                                                               VASNLQDEELCGGLWRLVLAQRWMERLKTVAGSKMQGLLERVNTEIHFVTKCAFQPPPSC
                                                                                                                                                                                                                                                                                                    MTVLAPAWSPNSSLLLLLLLLSPCLRGTPDCYFSHSPISSNFKVKFRELTDHLLKDYPVT
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                                                                                                                                       PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                    18986 MW;
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72.6%;
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Pred. No. 1.5
                                                                                                                                                                                                                                                                                                                                                 Score 578; DB 11;
Pred. No. 3.7e-49;
4; Mismatches 29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Craniata; Vertebrata; Euteleostomi;
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                                                                                                                                       PRT;
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                                      Tracheophyta;
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01-MAR-2001 (TrEMBLrel. 16, Cr
01-OCT-2001 (TrEMBLrel. 18, Lr
01-JUN-2002 (TrEMBLrel. 21, Lr
7--hable surface antigen p2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro: IPR000504; RNA_rec_mot.
Pfam; P000560; LRR; 6.
PRINTS; PR01582; KV33CHANNEL.
PRINTS; PR01217; PRICHEXTENSN.
SMART; SM00370; LRR; 5.
PROSITE; PS000030; RRM_RNP_1; UNKNOW
SEQUENCE 579 AA; 62607 MW; 0445
                                                                                                  STRAIN=FRIEDLIN;
Murphy L., Quail M., Harris D.,
Oliver K.;
                                                                        Submitted (AUG-2001) to the EMBL/GenBank/DDBJ EMBL; AL390114; CAC02038.2; -.
                                                                                                                                                                          Leishmania major.
Eukaryota; Euglenozoa;
              PRINTS;
                          Pfam; PF00560; LRR; 6.
                                                InterPro; IPR000561; EGF-like.
InterPro; IPR001611; LRR.
                                                                                                                                                                                                                                                                              Q9GY11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Oryza sativa nipponbare(GA3) genomic DNA, chromosome clone:P0406H10.";
                                    InterPro; IPR002965;
                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                            NCBI_TaxID=5664;
                                                                                                                                                                                                     LM12.156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases EMBL; APO02524; BAB07956.1; -. EMBL; APO03118; BAB33013.1; -. InterPro; IPR001611; LRR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sasaki T., Matsumoto T., Yamamoto K.;
"Oryza satra nipponbare(GA3) genomic DNA,
clore.orill7, nos "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=CV. NIPPONBARE; Sasaki T., Matsumoto T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=CV. NIPPONBARE;
Sasaki T., Matsumoto T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         clone:0J1174_D05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR003592; LRR_out.
InterPro; IPR002965; P_rich_extensn.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            [1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                          392 PSPPPP---
                                                                                                                                                                                                                                                                                                                                                              180 TAPOPPLLLLLLPVGLLLLAAAWCLHWQRTRRRTPRPGEQVPPVPSP 227
                                                                                                                                                                                                                                                                                                                                                                                          342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        244 ILLINTGLS------SCLPPEVGM-LREVTVF------
                                                                                                                                                                                                                                                                                                                                                                                                                                       283 VAGMRKVEQL-DVAHNLLTGAIPQAVCELPRLKNFTFAYNFFTGEPPSCAHAVPRYGDRR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17 LLLLSSGLSGTQDCSFQHSPISSDFAVKIRELSDYLLQDYPVTVASNLQDEELCGGLWRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  77
                                                                                                                                                                                                                                                                                                                                                                                        NCLPNRPAQRTLRQCAAF-----FARPPVNCAAFQCKPFVPALPPPSPPPP--SPPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                      VLAQRWMERLKTVAGSKMQGLLERVNTEIHFVTKCAFQ------PPPSCLRFV-----QT 125
                                                                                                                                                                                                                                                                                                                                                                                                             NI--SRLLQETSEQLVALKPWITRQNFSR----CLELQCQPDSSTLPPPWSPRPLEATAP
 SM00181; E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (JUN-2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                             PRELIMINARY;
 ; PRICHEXTENSN EGF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RRM_RNP_1; UNKNOWN_1.
.; 62607 MW; 04457E18E7405AAF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9.1%;
23.7%;
                                   P_rich_extensn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ť
                                                                                                                                                                          Kinetoplastida;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28;
                                                                                                                                                                                                                         Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                  Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 112.5; DB 10; Pred. No. 0.013;
                                                                                                                                                                                                                                                                            PRT;
                                                                                                            Rajandream M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                            668 AA
                                                                                                                                                                                                                                                                                                                                         -SPPPPSTSPPPPSP
                                                                                                                                                                         Trypanosomatidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          69;
                                                                                    databases
                                                                                                            Ivens A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -DVSFNRLAGPLPSA 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length
                                                                                                                                                                                                                                                                                                                                         411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1,
                                                                                                             Barrell
                                                                                                                                                                          Leishmania.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BAC
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RESULT 10
Q9GY33
ID Q9GY3
AC Q9GY3
DT 01-MA
DT 01-MA
DT 01-J(
DE PROB-
GN LM12
OS LE1S
OC EUR
OC STR
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                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local S
Matches 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (AUG-2001) to the EMBL/GenBank/DDBJ EMBL; AL390114; CAC02017.2; InterPro; IRR000561; EGF-like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Murphy L., Quail M., Oliver K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR002965; P_rich_extensn.
Pfam; PF00560; LRR; 7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRINTS; PR01217; PRICHEXTENSN SMART; SM00181; EGF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=FRIEDLIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Euglenozoa; Kinetoplastida;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAR-2001 (TrEMBLrel. 16,
01-OCT-2001 (TrEMBLrel. 18,
01-JUN-2002 (TrEMBLrel. 21,
01-JUN-2002 (TrEMBLrel. 21,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q9GY33 PRELIMINARY;
Q9GY33;
01-MAR-2001 (TrEMBLrel.
01-OCT-2001 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR001611;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=5664;
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VSGTLPPEWSSMGSLANLQLSLTQVSGTLPPQWSSMKKLTQLLLTDTLLSGTLPAEW 345
                                                                                                                                                                                                                                                                                                   LPPEWSSMPNLNAVELKRLKLSGT------LPADWS-SLKSLSNVVLEDMPIT----
                                                                                                                                                                                                                                                                                                                                                  LAPAWSPTTYLLLLLLSSGLSGTQDCSFQHSPISSDFAVKIRELSDYLLQDYPVTVASN 63
                                               DSSTLPPPWSPR-----PLEATAPTAPQPP-----LLLLLLLPVGLL--LLAAAW 203
                                                                                              ALRELTLDGTNLSGTLPPOWSAMASVISLNLEGTEVSGTLPPEWISMSRL-QTLNLRRTK 288
                                                                                                                                                  CLRFVQ---TNISRLLQ-----
                                                                                                                                                                                                                                                    LQDEELCGGLWRLVLAQRWMERLKTVAGSKMQGLLERVNTEIHFVTKCAFQPPP-----S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VSGTLPPEWSSMGSLANLQLSLTQVSGTLPPQWSSMRKLTQLLLTDTLLSGTLPAEW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DSSTLPPPWSPR-----PLEATAPTAPQPP-----LLLLLLPVGLL--LLAAAW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ALRFLTLDGTNLSGTLPPQWSAMASVISLNLEGTEVSGTLPPKWISMSRL-QTLNLRRTK 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLRFVQ---TNISRLLQ-------ETSEQLVALKP-WITRQNFSRCLELQCQP 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LPPEWSSMPNLQTLQVRRLKLSGT-----LPADWS-SLKSLSNVVLEDMPIT----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LQDEELCGGLWRLVLAQRWMERLKTVAGSKMQGLLERVNTEIHFVTKCAFQPPP----S
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AA;
                                                                                                                                                                                                    LPPEW--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          68470 MW; 8EB78AC101E01286 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                           8.3%;
26.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LRR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Harris D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8.4%; Score 104.5;
26.6%; Pred. No. 0.0
                                                                                                                                                                                                                                                                                                                                                                                                      20;
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                                                                                                                                                                                                                                                                                                                                                                                                    Score 102.5; D
Pred. No. 0.14;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Last sequence update)
Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rajandream M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
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                                                                                                                                                ETSEQLVALKP-WITRONFSRCLELQCQP 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -GSLERIQQLVLRKLKLTGPLPPQWSPMK 229
                                                                                                                                                                                                    GSLERIQQLVLRKLKVTGPLPPQWSPMK 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         648
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     update)
                                                                                                                                                                                                                                                                                                                                                                                                 77;
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                                                                                                                                                                                                                                                                                                                                                                                                      77;
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                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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RESULT Q8VIM6

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RESULT 12
Q9N753
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Best Local :
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Submitted (AUG-2001) to the EMEL; AL390114; CAB98658.2; -. InterPro; IPR001611; LRR. InterPro; IPR003592; LRR_out. Pfam; PF00560; LRR; 3. SMART; SM00370; LRR; 3.
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01-MAR-2002
01-JUN-2002
                                                             Murphy L., Quail M., Oliver K.;
                                                                                                              Leishmania major.
Eukaryota; Euglenozoa;
NCBI_TaxID=5664;
                                                                                                                                                                01-OCT-2001 (TrEMBLrel. 01-DEC-2001 (TrEMBLrel.
                                                                                                                                                                                                           Q9N753
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AF3/22, MGD; MGI:2153816;
                                                                                  STRAIN-FRIEDLIN,
                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                        Probable surface
                                                                                                                                                                                               Q9N753;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Verpy E., Masmoudi S., Zwaenepoel I., Del Castillo I., Nouaille S., Blanchar Moreno F., Mueller R.F., Petit C.; "Mutations in a new gene encoding a pron-syndromic deafness at the DFNB16 l
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q8VIM6;
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AF375593; AAL35321.1; -
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(TrEMBLrel.)
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23.7%;
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Pred. No.
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Blanchard S., Laine
                                                                      Rajandream M.,
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RESULT
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Q9C5T0
Q9C5T0;
01-JUN-2001
01-JUN-2001
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01-MAR-2001
01-DEC-2001
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                                                                                                                                                                                                     spliced transcript.";
Virus Res. 69:119-130(2000).
EMBL; AF232689; AAF99111.1;
                                                                                                                                                                                                                                                                                            "Complete J. Virol.
                                                                                                                                                                                                                                                                                                                                                                       Rat cytomegalovirus (strain Maastricht)
Viruses; dsDNA viruses, no RNA stage; H
Betäherpesvirinae; Muromegalovirus.
                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                   "Rat cytomegalovirus R89 is
                                                                                                                                                                                                                                                  STRAIN=MAASTRICHT;
MEDLINE=20473137; PubMed=11018281;
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                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=79700;
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                                                                                              AWCLHWQRTRRRTPRPGEQVPPVPSPQD 229
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                                                                            -QATRASPRPETDAPP-PTPAD
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33.0%;
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23.8%;
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s a highly conserved
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Pred. No. 0
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01-MAR-2002 (TrEMBLrel. 20, Last annotation update)

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01-JAN-1998 (TrEMBLrel.
01-JAN-1998 (TrEMBLrel.
01-MAR-2002 (TrEMBLrel.
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SMART; SM00220; S_TKC; 1.
SMART; SM00219; TyrKC; 1.
PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
ATP-binding; Kinase; Transferase.
SEQUENCE 658 AA; 72991 MW; DCF9CF5F1748F614 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Identification of genes encoding receptor-like protein kinases as possible targets of pathogen- and salicylic acid-induced WRKY DNA-binding proteins in Arabidopsis."; plant J. 24.837-847(2000).
EMBL; AF224/05; AAK28315.1; -.
"Genome sequence of the nematode C.elegans: investigating biology."; Science 282.2012-2018(1998).
EMBL; Z81546, CAB04464.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR001245; Tyr_pkinase. Pfam; PF01657; DUF26; 2. Pfam; PF00069; pkinase; 1.
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                               SEQUENCE FROM N.A. MEDLINE=99069613; PubMed=9851916;
                                                                                                                                                                                                                                           SEQUENCE FROM N.A. Barlow K.;
                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
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Interpro; IPR000719; Euk_pkinase.
Interpro; IPR002290; Ser_thr_pkinase.
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                                                                                                            none;
                                                                                                                                                                                                                  Submitted (NOV-1996)
                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=6239;
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Last sequence update)
Last annotation update)
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Query Match
Best Local Similarity
***ches 38; Conserva
Search completed: November 24, Job time: 31.2232 secs
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InterPro; IPR000242; Tyr_Pr
Pfam; PF00102; V_phosphatase; 1.
SMART; SM00194; PTFc; 1.
SMART; SM00194; PTFc; 1.
PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.
PROSITE; PS00056; TYR_PHOSPHATASE_2; 1.
PROSITE; PS50055; TYR_PHOSPHATASE_PTP;
PROSITE; PS50055; TYR_PHOSPHATASE_PTP;
                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                Hydrolase.
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                                                                                                                                         683
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                                                                                                     192 LPVGLLLLAA-----AWCLHWQRTRRRTPRPGEQVPPVPSP
                                                                                                                                                                                                          627 MDAVKAVDGTKYSSVIDALEKLSTMDLDFQKYKFKEAPATLKAMDL----FFASYASNLA 682
                                                                                                                                                                                                                                         83 MERLKTVAGSKMQGL---LERVNTEIHFVTKCAFQPPPSCLRFVQTNISRLLQETSEQLV 139
                                                                     GAVGGLLVVAIIGVILFFVFFQKKKKKEDKPDD--PPAPLP
                                                                                                                                       ALRPOPTTSDPTAAAPVPIPNNKGSLNGNPSPSSPPLLPPVASSTPAATPEESNMLLYII 742
                                                                                                                                                                       ALKPWITRQNFSRCLELQCQPDSSTL---PPPWSPRPLEATAPTAP-----QPPLLLLLL
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Result
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2: /SIDS2/gcgdata/
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1242
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Copyright (c) 1993 - 2002 Compugen Ltd
                                                                                                                                                                                                                                                                                                                                           /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1989.DAT:*
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     AAR67541
AAW67769
AAY620192
AABB08129
AABB08129
AAB66175
AAR661791
AAW69007
                                                                                                                                                                                                                                              SUMMARIES
Human flt-3 ligand.
Human flt3-ligand.
Full length wild t
Human Flt-3 ligand
Human Flt3L polype
Human S86/S109 Flt
Human flt-3 ligand
Human flt-3 mutein
Human flt-3 recept
Mature wild type h
                                                                                                                                                                                            Description
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	AAW83294	19	313	9	735	U,
recep	AAW69052	19	144	9.	735	_
FLT4C	75	19	144	9.	735	w
n flt-3	90	19	140	9.	735	١٠
Human flt3 ligand	AAW77911	19	140	9.	735	
Trimeric Flt3L-G-C	AAW78008	19	523	9.	1.1	_
flt	AAW83286	19	349	9.	736.5	•
n flt	AAW83291	19	340	9.	1.1	w
L 1-1	AAW78005	19	349	9.	6.1	7
n flt	AAW83289	19	349	9.	4.1	٠,
an flt-3 recep	AAW69050	19	143	9.	739	Ο,
liga	AAW77926	19	143	9.	739	_
Chimeric receptor	AAW78124	19	377	9.	740.5	•
an flt-3	AAW69054	19	150	0	745	١٥
Flt3 ligand FLT10C	AAW77930	19	150	0	745	_
Mouse Flt-3 ligand	AAB20189	22	232	1.	764	_
Mouse MoT110/T118	AAR66177	16	232	-	768	•
Flt-3	AAB20186	22	231	1	768.5	w
ne flt3-	AAW67768	20	231		768.5	~
flt-3 1	AAR67540	16	231	-	768.5	٠,
matui	AAY58211	21	. 265	w	791.5	٠.
F1t-3	AAY58207	21	276	٠.	796.5	_
e mature	AAY58206	21	268	4	797.5	~
F1t-3 1	AAB20193	22	178	.7		
Flt-3 ]	AAY58210	21	291		894.5	
e Flt-3 ]	AAY58204	21	294		5	_
Flt-3 li		22	185		970	_
n flt-3	AAY69725	21	209	8	1100	ω
flt-3	•	21	209	9	1107	•
n flt-3	~	21	209	9	1108	٠.
n flt-3 mute	$\sim$	21	209	9.	1108	٠.
lt-3 mute	~	21	209	9	1110	-
lt-3 mute	$\mathbf{a}$	21	209	9.	1110	~
lt-3 mute	AAY69726	21	209	89.4	1110	
Human flt-3 mutein	AAY69723	21	209	9.	1110	•

## ALIGNMENTS

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RESULT 1
AAR67541
ID AAR6
                                                                 07-DEC-1994.
                                                                                                         Domain
                                                                                                                                         Key
                                                                                                                                                         Homo sapiens.
                                                                                                                                                                          Flt-3 ligand; flt3-L;
                                                                                                                                                                                         Human flt-3 ligand
                                                                                                                                                                                                           05-AUG-1995 (first entry)
                                                                                                                                                                                                                           AAR67541;
                                                                                                                                                                                                                                           AAR67541 standard; Protein; 235
19-MAY-1994;
                                EP627487-A.
                                                         Domain
                                                                        Domain
                                                                                                                                 Peptide
94EP-0303575
                                                                                                       /label= Sig_peptide /note= "signal peptide may extend to position 27..182
                                                         206
                                                                         183..205
                                                                              /label= Cytoplasmic_domain
                                                        /label= Transmembrane_domain
206..235
                                                                                                                                         location/Qualifiers
                                                                                                                                                                         anemia; cancer; AIDS; gene therapy
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                                                                                         start
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RESULT 2
AAW67769
ID AAW6
XX AAW6
AC AAW6
AC BAW6
XX AAW6
XX AAW6
XX AAW1
ID CONTROL
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03-DEC-1993;
07-MAR-1994;
11-MAY-1994;
                                                    17-JUN-1997;
                                                                                                 12-JUN-1998;
                                                                                                                                                23-DEC-1998
                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                 Antigen-specific peripheral immune tolerance; flt3-ligand; flt3-L;
                                                                                                                                                                                                                                                                                                                                                                                        Human flt3-ligand
                                                                                                                                                                                                                                                                                                                                                                                                                                          25-MAR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAW67769 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A human T-cell lambda-gtl0 random primed cDNA library was screened with a fragment corresponding to the extracellular domain of mouse flt3 ligand (flt3-L) (nt 103-516 of AAQ79076) to isolate human flt3-L cDNA. Flt-3 stimulates progenitor and
                                                                                                                                                                                                                                                                                            tissue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           stem
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                                                                                                                                                                                                                                                                                                                immunogenic; autoimmune disease; organ transplantation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ( VMMI)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    181 APQPPLLLLLLPVGLLLLAAAWCLHWQRTRRRTPRPGEQVPPVPSPQDLLLVEH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Sin
hes 235;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RFVQTNISRLLQETSEQLVALKPWITRQNFSRCLELQCQPDSSTLPPPWSPRPLEATAPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ASNLQDEELCGGLWRLVLAQRWMERLKTVAGSKMQGLLERVNTEIHFVTKCAFQPPPSCL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MTVLAPAWSPTTYLLLLLLLSGLSGTQDCSFQHSPISSDFAVKIRELSDYLLQDYPVTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REVQTNISRLLQETSEQLVALKPWITRQNESRCLELQCQPDSSTLPPPWSPRPLEATAPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ASNLQDEELCGGLWRLVLAQRWMERLKTVAGSKMQGLLERVNTEIHFVTKCAFQPPPSCL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cells,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MTVLAPAWSPTTYLLLLLLLSSGLSGTQDCSFQHSPISSDFAVKIRELSDYLLQDYPVTV
                                                                                                                                                                                                                                                                                         transplantation.
  IMMUNEX CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IMMUNEX CORP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MP, · Lyman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         235 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Page 29-30;
                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
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93US-0106463.
93US-0111758.
93US-0162407.
94US-0209502.
94US-0243545.
                                                    97US-0877421.
                                                                                                 98WO-US12085
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            be used e.g. in gene therapy protocols
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SD
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                                                                                                                                                                                                                               Immunomodulator; immunosuppressive; cytostatic; antianemic; anti-HIV; neuroprotective; antiallergic; flt3 ligand; flt3-L; wild type; allergy; cell surface tyrosine kinase receptor; hematopoietic progenitor cell; cellular expansion; cellular differentiation; natural killer cell; cancer; dendritic cell; immune response; autoimmunity; immunosuppression; myelodysplasia; aplastic anemia; HIV infection; lymphoma; neuroblastoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 or therapeutic molecule, respectively. The polypeptide is capable of binding the flt3 receptor and is: a) amino acids 28 x of murine flt3 ligand (flt3-L), where x is an amino acid between 163-231; b) amino acids 28-y of human flt3-L, where y is an amino acid between 160-235; and c) a polypeptide that has at least 90% identity to the polypeptides of either (a) or (b). The method ameliorates the effects of autoimmune diseases, food allergies or organ or tissue rejection following transplantation. Administration of flt3-L allows lower doses of antigens to be used in vivo for mucosally administered antigens. The present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A method has been developed of initiating or enhancing: (i) an antigen-
specific immune tolerance; or (ii) immunotolerance of a therapeutic
immunogenic molecule by addition of a polypeptide, before, after or with
the mucosal administration of an immunotolerising amount of the antigen
                                                                                                                                                                                                          myelodysplasia; aplastic anemia;
multiple myeloma; leukemia.
                                                                                                                                                  Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                               Full length wild type human flt-3 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         05-JUL-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sequence represents human flt3-L.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              standard; Protein;
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Pred. No. 5e-109;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to novel soluble flt3 ligand (flt3-L) polypeptides which exhibits increased or decreased biological activity relative to the full length wild type (this sequence) or mature (AAY69720) flt3-L polypeptides. The flt3-L protein binds cell surface tyrosine kinase receptors and regulate growth and differentiation of hematopoietic progenitor cells. The flt3-L protein can be used to induce cellular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mutant soluble flt3 ligand polypeptide used in cellular expansion, immune response stimulation or treatment of pathological condition contains amino acid substitutions at positions 8, 84, 118 or 122
                                              Flt-3 ligand; Fms-like tyrosine kinase; human; vaccine;
immunotherapy; therapy; tumour; cancer; melanoma; glion
lymphoma; autoimmune disease; infection; gene therapy.
                                                                                                                 Human Flt-3 ligand
                                                                                                                                                                                    AAB20192;
                                                                                                                                                                                                                    AAB20192 standard; Protein; 235 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ovarian cancer, lymphoma, multiple myeloma, neuroblastoma or acute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               enhance a patient's immune response and can be used to treat an immune disorder (e.g. allergy, autoimmunity or immunosuppression). The protein may be used to treat a pathological condition e.g. myelodysplasia aplastic anemia, HIV infection, breast, small cell lung, testicular or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                expansion (especially in vivo) or differentiation, e.g. in hematopoletic, natural killer (NK) or dendritic cells, especially in the presence of growth factors such as interleukins, colony stimulating factors or protein kinases. The protein can also modulate, augment or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; Page 72-73;
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                                                                                                                                               entry)
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Pred. No. 5e-109;
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Best Local :
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                                                                                                                                                                                                                                              suppressing tumour growth in a mammal. The tumour is melanoma, glioma or lymphoma, particularly B-cell lymphoma. They can also be used for the prophylactic and/or therapeutic treatment of:
(a) bacterial (e.g. Bacillus infections), viral (e.g. hepatitis B and C in humans), parasitic (e.g. malaria) and fungal infections; (b) autoimmune diseases (e.g. rheumatoid arthritis and osteoarthritis); (c) cancer; and (d) Aujeszky's disease in pigs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (Flt-3 ligand). The invention is directed to enhancing the immune response of a vertebrate to an antigen or a cytokine by administering in vivo, into a tissue of a vertebrate, a Flt-3 ligand-encoding polynucleotide, and I or more antigen or cytokine-encoding polynucleotides. The Flt-3 ligand-encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Immunogenic compositions comprising Flt-3 ligand encoding polynucleotide and one or more antigen, or cytokine encoding polynucleotides, useful for suppressing tumour growth and for treating
                                                                                                                             Sequence
                                                                                                                                                                                                                       Various other examples of these diseases are given in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               compositions comprising the polynucleotides are useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present sequence is that of human Fms-like tyrosine kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 2; Page 132-133; 149pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            autoimmune diseases (e.g. rheumatoid arthritis)
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      235;
                                 Similarity
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                                                                                                                             ĀΑ;
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27..182
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27..235
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      0,
Score 1242; DB 22
Pred. No. 5e-109;
; Mismatches 0;
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                                                                                                                                                                                             CC The invention relates to treating an individual at risk for or suffering CC from infection with a pathogenic or opportunistic organism. The method CC involves administering a combination of two to five agents comprising: CC (a) dendritic cell mobilisation factor; (b) dendritic cell maturation CC agent; (c) dendritic cell activation agent; (d) T cell enhancing factor; CC or (e) activated, antigen-specific T cells. The methods are useful for CC treating an individual at risk for or suffering from infection with a CC (e.g. M. tuberculosis), yeast, fungi (e.g. Viruses (e.g. HIV), bacteria CC (e.g. M. tuberculosis), yeast, fungi (e.g. C. albicans) or protozoa (e.g. CC T. cruzi, which causes Chaga's disease). The methods are especially CC useful for treating an individual suffering from immunosuppression by CC enhancing a lymphocyte-mediated immune response. In particular, the CC method is useful for treating inflammations, chickenpox, oral or genital CC herpes, mononucleosis, multifocal leukoencephalopathy, hepatitis, AIDS, C T cell leukemia or T cell lymphoma. The activated antigen-presenting CC dendritic cells are useful as a vaccine adjuvant. The present sequence CC represents a human Filti. no lymphotypent of the present sequence
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                                                                      Matches
                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          chickenpox or AIDS, by administering a combination of dendritic cell mobilization factor or maturation agent, T cell enhancing factor and antigen-specific T cells -
                                                                                                                                         Sequence
                                                                                                                                                                        represents a human Flt3L polypeptide fragment, that can be used as a dendritic cell mobilisation factor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Page 37-38; 43pp;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lynch DH,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Dendritic cell; mobilisation factor; T cell; adjuvant; antibacterial; fungicide; protozoacide; virucide; anti-inflammatory; anti-HIV; tuberculostatic; cytostatic; human; Flt3L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human Flt3L polypeptide
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                                                                    100.0%; llarity 100.0%; Conservative
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Pred. No. 5e-
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RESULT 6
AAR66175
ID AAR6
C A cDNA Library Irou Lie numes screened.

C pME185, was screened with an 800 bp fragment derived from mouse clone T118. This fragment encompasses the coding region conserved between two mouse clones, T118 and T110. Approx. 20 conserved between two mouse clones, T118 and T110. Approx. 20 conserved between two mouse clones, T118 and T110. Approx. 20 colones, S86 and S109, were found to be approx. 75% homologous to the mouse clones over the first 163 AAs. Clone S86 continued to show homology to T110 until the stop codon, although to a closes r degree, for an overall homology of 66%. Clones T118 and C1 lesser degree, for an overall homology of 66%. Clones T118 and C2 after mouse residue 163 (human residue 160). An additiona mouse clone designated M58 has a 29 AA insert at the junction between cc the common and divergent portions of the mouse ligand.
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07-JUL-1993;
16-JUL-1993;
13-AUG-1993;
24-AUG-1993;
19-NOV-1993;
                                                                                                                                                                                                                                                                                                                                                                    New ligand for the FIt3 tyrosine kinase receptor - and related nucleic acid, vectors, host cells and antibodies, useful for treating abnormal cell physiology and proliferation, e.g. cancer, also for diagnosis and drug screening
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (INRM
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                                                                                                                                                                                                                                                                                                                            Claim 11; Page 76-77; 90pp; English.
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93US-0089263.
93US-0092549.
93US-0106340.
93US-0112391.
93US-0155111.
93US-0162413.
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                                                    Immunogenic compositions comprising Flt-3 ligand encoding polynucleotide and one or more antigen, or cytokine encoding polynucleotides, useful for suppressing tumour growth and for autoimmune diseases (e.g. rheumatoid arthritis).
The present sequence is that of human Fms-like tyrosine (Flt-3 ligand). The invention is directed to enhancing
                                Claim 2; Page 137-138; 149pp; English.
                                                                                                                                                                                       30-JUL-1999;
                                                                                                                                                                                                           31-JUL-2000; 2000WO-US20679
                                                                                                                                                                                                                                                                                       Domain
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                                                                                                                                                                                                                                                                                                                                                      Protein
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                                                                                                            2001-123319/13.
DB; AAF30312.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APQPPLLLLLLPVGLLLLAAAMCLHWQRTRRRTPRPGEQVPPVDSPQDLLLVEH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ASNLQDEELCGGLWRLVLAQRWMERLKTVAGSKMQGLLERVNTEIHFVTKCAFQPDPSCL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RFVQTNISRLLQETSEQLVALKPWITRQNFSRCLELQCQPDSSTLPPPWSPRPLEATAPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RFVQTNISRLLQETSEQLVALKPWITRQNFSRCLELQCQPDSSTLPPPWSPRPLEATAPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APQPPLLLLLLPVGLLLLAAAWCLHWQRTRRRTPRPGEQVPPVPSPQDLLLVEH 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ASNLQDEELCGALWRLVLAQRWMERLKTVAGSKMQGLLERVNTEIHFVTKCAFQPPPSCL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MTVLAPAWSPTTYLLLLLLSSGLSGTQDCSFQHSPISSDFAVKIRELSDYLLQDYPVTV
                                                                                                                                                                                                                                                                                                                                                                                                                                autoimmune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                    therapy; tumour; cancerion; gene
                                                                                                                                                                                       99US-0146170
                                                                                                                                                                                                                                                                                                                                         /label=
27..235
/label=
                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                       206
                                                                                                                                                                                                                                                                                              /label= Transmembrane_domain
                                                                                                                                                                                                                                                                         /label= Cytoplasmic_domain
                                                                                                                                                                                                                                                                                                                   /label=_Extracellular_domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99.5%;
                                                                                                                                                                                                                                                                                                                                        Mature_protein
                                                                                                                                                                                                                                                                                                                                                              Signal_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AΑ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1236;
No. 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 16;
L.8e-108;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length
          kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            235;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
                                                                treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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AAY69721
ID AAY
XX
AC AAY
XX
AC AAY
XX
DT 05-
XX
Inm
AX
Inm
KW Inm
KW cell
KW cell
KW cell
KW mye
KW mul
XX
OS Hon
OS Syr
XX
PN WOZ
XX
PD 13-
XX
PP 25-
XX
PR 02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QΥ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 234; Conserv
                                                                                                                                                                                                                                 Immunomodulator; immunosuppressive; cytostatic; antianemic; anti-HIV; neuroprotective; antiallergic; flt3 ligand; flt3-L; wild type; allergy; cell surface tyrosine kinase receptor; hematopoletic progenitor cell; cellular expansion; cellular differentiation; natural killer cell; cancer; dendritic cell; immune response; autoimmunity; immunosuppression myelodysplasia; aplastic anemia; HIV infection; lymphoma; neuroblastoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              antigens or cytokines is produced in vivo. Pharmaceutical compositions comprising the polynucleotides are useful for suppressing tumour growth in a mammal. The tumour is melanoma, glioma or lymphoma, particularly B-cell lymphoma. They can also be used for the prophylactic and/or therapeutic treatment of:

(a) bacterial (e.g. Bacillus infections), viral (e.g. hepatitis I and C in humans), parasitic (e.g. malaria) and fungal infections (b) autoimmune diseases (e.g. rheumatoid arthritis and various other examples of these diseases are given in the
                                                      25-JUN-1999;
                                                                                           13-JAN-2000
                                                                                                                                WO200001823-A2
                                                                                                                                                                 Synthetic.
                                                                                                                                                                                                                       multiple myeloma; leukemia; mutein.
                                                                                                                                                                                                                                                                                                                                                                       Human flt-3 mutein L-3H.
                                                                                                                                                                                                                                                                                                                                                                                                            05-JUL-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              immune response of a vertebrate to an antigen or a cytokine by administering in vivo, into a tissue of a vertebrate, a Flt-3 ligand-encoding polynucleotide, and 1 or more antigen- or cytokine-encoding polynucleotides. The Flt-3 ligand-encoding polynucleotide may encode the present full-length human Flt-3 ligand polypeptide, or amino acids 27-185, 1-185, 27-235 or 1-235 of the Flt-3 ligand. The polynucleotides are incorporated into
                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAY69721 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     of the flt-3 ligand. The polynucleotides are incorporated into the cells of the vertebrate in vivo, and a prophylactically or therapeutically effective amount of flt-3 ligand and 1 or more
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         specification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APQPPLLLLLLLPVGLLLLAAAWCLHWQRTRRRTPRPGEQVPPVPSPQDLLLVEH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RFVQTNISRLLQETSEQLVALKFWITRQNFSRCLELQCQPDSSTLPPPWSPRPLEATAPT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MTVLAPAWSPTTYLLLLLLLSGLSGTQDCSFQHSPISSDFAVKIRELSDYLLQDYPVTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APQPPLLLLLLPVGLLLLAAAWCLHWQRTRRRTPRPGEQVPPVPSPQDLLLVEH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REVQTNISRLLQETSEQLVALKPWITRQNESRCLELQCQPDSSTLPPPWSPRPLEATAPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ASNLQDEELCGGLWRLVLAQRWMERLKTVAGSKMQGLLERVNTEIHFVTKCAFQPPPSCL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ASNLQDEELCGALWRLVLAQRWMERLKTVAGSKMQGLLERVNTEIHFVTKCAFQPPPSCL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MTVLAPAWSPTTYLLLLLLLSSGLSGTQDCSFQHSPISSDFAVKIRELSDYLLQDYPVTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    235 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                      99WO-US14296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No. 1.80
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 1236;
Pred. No. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .8e-108;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               infections;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             235;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               235
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          120
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0;

02-JUL-1998;

98US-0109100

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RRESULT 9
AAW69007
ID AAW6
XX
AC AAW6
XX
AC AAW6
XX
Huma
KW Huma
KW Huma
KW Grug
KW Grug
KW Gen
KW Gen
XX
KW Hone
KW Gen
XX
KW Home
XX
XX
Home
XX
XX
XX
XX
XX
XX
                                                                                                                                                                                                                                                                                                                                                                                                                                                               DЬ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Qy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DЬ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QΥ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Вb
                                                                                                                                                                                                                                                                                                                                                                                                                          γQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       colony stimulating factors or protein kinases. The protein can also modulate, augment or enhance a patient's immune response and can be used to treat an immune disorder (e.g. allergy, autoimmunity or immunosuppression). The protein may be used to treat a pathological condition e.g. myelodysplasia, aplastic anemia, HIV infection, breast, small cell lung, testicular or ovarian cancer, lymphoma, multiple
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              binds cell surface tyrosine kinase receptors and regulate growth and differentiation of hematopoletic progenitor cells. The flt3-L protein can be used to induce cellular expansion (especially in vivo) or differentiation, e.g. in hematopoletic, natural killer (NK) or dendritic cells, especially in the presence of growth factors such as interleukins,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to novel soluble flt3 ligand (flt3-L) polypeptides which exhibits increased or decreased biological activity relative to the full length wild type (AAY69719) or mature (AAY69720) flt3-L polypeptides. This sequence represents an example of the novel flt-3 ligands and comprises the L-3H mutant polypeptide. The flt3-L protein
                                                                                                      bone marrow reconstitution; haematological disease; immune deficiency; drug-induced myelosuppression; renal dialysis; gene therapy; infection congenital metabolic disease; neurological disease; therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Graddis TJ,
                  W09818923-A1
                                                                                                                                                                                                                                   01-OCT-1998
                                                                                                                                                                                                                                                                                                        AAW69007 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (IMMV ) IMMUNEX CORP
                                                    Homo sapiens.
                                                                                       dendritic cell
                                                                                                                                                                                              Human flt-3 receptor agonist
                                                                                                                                                                                                                                                                                                                                                                                                182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      145
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ocal Similarity
                                                                                                                                                                                                                                                                                                                                                                                                LHWQRTRRRTPRPGEQVPPVPSPQDLLLVEH
                                                                                                                                                                                                                                                                                                                                                                                                              LHWQRTRRRTPRPGEQVPPVPSPQDLLLLVEH 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ITRONFSRCLELQCOPDSSTLPPPWSPRPLEATAPTAPOPPLLLLLLLLPVGLLLLAAAWC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ITRQNFSRCLELQCQPDSSTLPPPWSPRPLEATAPTAPQPPLLLLLLLLPVGLLLLAAAWC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RLKTVAGSKMQGLLERVNTEIHFVTKCAFQPPPSCLRFVQTNISRLLQETSEQLVALKPW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RLKTVAGSKMQGLLERVNTEIHFVTKCAFQPPPSCLRFVQTNISRLLQETSEQLVALKPW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SGTQDCSFQHSPISSDFAVKIRELSDYLLQDYPVTVASNLQDEELCGGLWRLVLAQRWME 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  211;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               soluble flt3 ligand polypeptide used in cellular expansion, response stimulation or treatment of pathological conditions ns amino acid substitutions at positions 8, 84, 118 or 122 -
                                                                                                                                                            flt-3 receptor agonist; haematopoietic cell stimulation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          neuroblastoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       212 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           McGrew
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               79-80; 90pp; English
                                                                                       production
                                                                                                                                                                                                                                                                                                      peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  90.5%;
100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          acute
                                                                                                                                                                                                                                                                                                        209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 1124; DB 21;
Pred. No. 5.9e-98;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Leukemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   212;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
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RESULT 10
AAY69720
ID AAY69
XX
AC AAY69
XX
DT 05-JU
XX
DE Matur
XX

AAY69720; AAY69720

standard;

Protein;

209

ĄΑ

05-JUL-2000

(first entry)

Mature wild type human flt-3 protein

밁 QΥ Вþ Qy

147

RQNFSRCLELQCQFDSSTLPPPWSPRPLEATAPTAPQPPLLLLLLLLPVGLLLLAAAWCLH KTVAGSKMQGLLERVNTEIHFVTKCAFQPPPSCLRFVQTNISRLLQETSEQLVALKPWIT KTVAGSKMQGLLERVNTEIHFVTKCAFQPPPSCLRFVQTNISRLLQETSEQLVALKPWIT 146

120

0

RQNFSRCLELQCQFDSSTLPPPWSPRPLEATAPTAPQPPLLLLLLLPVGLLLLAAAWCLH

180

61 87

망 QΥ

181 207 121

WORTRRTPRPGEQVPPVPSPQDLLLVEH WORTERFERPGEOVPPVPSPQDLLLVEH 235

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                                                                                                                                                   γ
                                                                                                                                                                              This sequence represents a rearranged human flt-3 receptor agonists of CC the invention. The agonists have a modified flt-3 ligand amino acid CC sequence. The agonists are used to stimulate production of haematopoietic CC cells in vivo (e.g. in a subject about to donate blood) or for ex vivo CC expansion for subsequent transplantation, e.g. to reconstitute bone CC marrow after chemotherapy, disease etc., or to treat haematological CC disease such as drug-induced myelosuppression, defects caused by CC infections, burns or renal dialysis. Optionally ex vivo expanded cells CC are transduced with a gene therapy vector for treating e.g. congenital CC metabolic diseases, immune deficiency, neurological disease, cancer and CC infections. The agonists can also be used in the treatment of tumours, CC infections and autoimmune disease, when administered optionally with an CC antigen. The agonist can also be used in the production of dendritic CC cells for use as an immunising adjuvant for treatment disorders including acquired immune deficiency syndrome. Compared with native ligands, the CC new agonists have better stimulatory activity, reduced side effects CC and/or better physical properties such as solubility, stability or refold CC efficiency. When used together with other stimulatory agents, the
                                                                          Matches
                                                                                          Query Match
Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rearranged flt-3 receptor agonists and nucleic acids encoding them used to stimulate production of haematopoietic and dendritic cells, for treatment of haematological diseases, bone marrow reconstitution
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Staten NR, Streeter PR,
                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Page 9-10; 158pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      and in gene therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Feng Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23-OCT-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (SEAR ) SEARLE & CO G
                                       27
Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       McKearn JP,
                                                                                                                                                   209 AA;
                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       97WC-US18700
                                                                                          89.7%; Score 1114; DB 19; 100.0%; Pred. No. 5.1e-97;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       McWherter
R, Woulfe
                                                                            0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CA,
                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Minnerly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         JC,
                                                                            0;
                                                                                                             Length 209;
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                                                                            Gaps
   60
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The invention relates to novel soluble flt3 ligand (flt3-L) polypeptides which exhibits increased or decreased biological activity relative to the full length wild type (AAY69719) or mature (this sequence) flt3-L colypeptides. The flt3-L protein binds cell surface tyrosine kinase creeptors and regulate growth and differentiation of hematopoietic progenitor cells. The flt3-L protein can be used to induce cellular cells expansion (especially in vivo) or differentiation, e.g. in cellular cells expansion (especially in vivo) or differentiation, e.g. in the cellular cells expecially in the cellular (NK) or dendritic cells, especially in the cellular cells or protein kinases. The protein can also modulate, augment or cellular (e.g. allergy, autoimmunity or immunosuppression). The protein cellular (e.g. allergy, autoimmunity or immunosuppression). The protein cellular (e.g. allergy, autoimmunity or immunosuppression). The protein cellular cellular or ovarian cancer, lymphoma, multiple myeloma, neuroblastoma or acute
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mutant soluble flt3 ligand polypeptide used in cellular expansion, immune response stimulation or treatment of pathological conditions contains amino acid substitutions at positions 8, 84, 118 or 122 -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (IMMV ) IMMUNEX CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    02-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25-JUN-1999;
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   181
                                                            207
                                                                                                                  121
                                                                                                                                                                        147
                                                                                                                                                                                                                                 61
                                                                                                                                                                                                                                                                                          87
                                                                                                                                                                                                                                                                                                                                                                                                         27
                              WQRTRRRTPRPGEQVPPVPSPQDLLLVEH
                                                                                                                                                                                                                                                                                                                                                               TQDCSFQHSFISSDFAVKIRELSDYLLQDYPVTVASNLQDEELCGGLWRLVLAQRWMERL
WQRTRRRTPRPGEQVPPVPSPQDLLLVEH
                                                                                                      RQNFSRCLELQCQPDSSTLPPPWSPRPLEATAPTAPQPPLLLLLLLPVGLLLLAAAWCLH
                                                                                                                                    RONFSRCLELQCQPDSSTLPPPWSPRPLEATAPTAPQPPLLLLLLLPVGLLLLLAAAWCLH
                                                                                                                                                                                                                  KTVAGSKMQGLLERVNTEIHFVTKCAFQPPPSCLRFVQTNISRLLQETSEQLVALKPWIT
                                                                                                                                                                                                                                                                        KTVAGSKMQGLLERVNTEIHFVTKCAFQPPPSCLRFVQTNISRLLQETSEQLVALKPWIT
                                                                                                                                                                                                                                                                                                                                 TQDCSFQHSPISSDFAVKIRELSDYLLQDYPVTVASNLQDEELCGGLWRLVLAQRWMERL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2000-182115/16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               209;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1; Page 89-90; 90pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              98US-0109100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 89.7%;
100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 1114; DB 21;
Pred. No. 5.1e-97;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                   235
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               209;
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RESULT 11 AAY69723

Qy

147

RQNFSRCLELQCQPDSSTLPPPWSPRPLEATAPTAPQPPLLLLLLLPVGLLLLAAAWCLH

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Qy DЪ Ωy DЬ δÃ В δÃ

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В
                                    Qy
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                                                                                                                                          Matches
                                                                                                                                                          Query Match
Best Local
                                                                                                                                                                                                                                                 polypeptides. This sequence represents an example of the novel flt-3 ligands and comprises the K04E mutant polypeptide. The flt3-L protein binds cell surface tyrosine kinase receptors and regulate growth and differentiation of hematopoietic progenitor cells. The flt3-L protein can be used to induce cellular expansion (especially in vivo) or differentiation, e.g. in hematopoietic, natural killer (NK) or dendritic cells, especially in the presence of growth factors such as interleukins, colony stimulating factors or protein kinases. The protein can also modulate, augment or enhance a patient's immune response and can be used to treat an immune disorder (e.g. allergy, autoimmunity or immunosuppression). The protein may be used to treat a pathological condition e.g. myelodysplasia, aplastic anemia, HIV infection, breast, mualcama aniarchiastoma or sorted leukomia.
                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to novel soluble flt3 ligand (flt3-L) polypeptides which exhibits increased or decreased biological activity relative to the full length wild type (AAY69719) or mature (AAY69720) flt3-L the full length wild type (AAY69719) or mature (AAY69720)
                                                                                                                                                                                                                                           myeloma, neuroblastoma or acute leukemia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mutant soluble flt3 ligand polypeptide used in cellular expansion, immune response stimulation or treatment of pathological conditions contains amino acid substitutions at positions 8, 84, 118 or 122 -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cancer; dendritic cell; immune response; autoimmunity; immunosuppression; myelodysplasia; aplastic anemia; HIV infection; lymphoma; neuroblastoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2000-182115/16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Graddis TJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (IMMV ) IMMUNEX CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                02-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Immunomodulator; immunosuppressive; cytostatic; antianemic; anti-HIV; neuroprotective; antiallergic; flt3 ligand; flt3-L; wild type; allergy; cell surface tyrosine kinase receptor; hematopoletic progenitor cell; cellular expansion; cellular differentiation; natural killer cell;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25-JUN-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAY69723 standard; Protein;
     61
                                                                                                          27
                                                                                  TQDCSFQHSPISSDFAVKIRELSDYLLQDYPVTVASNLQDEELCGGLWRLVLAQRWMERL
                  KTVAGSKMQGLLERVNTEIHFVTKCAFQPPPSCLRFVQTNISRLLQETSEQLVALKPWIT
KTVAGSKMQGLLERVNTEIHFVTECAFQPPPSCLRFVQTNISRLLQETSEQLVALKPWIT
                                                                  TQDCSFQHSPISSDFAVKIRELSDYLLQDYPVTVASNLQDEELCGGLWRLVLAQRWMERL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sapiens.
                                                                                                                                                         Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      myeloma;
                                                                                                                                                                                                           209
                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            McGrew JT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        84-85;
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                                                                                                                                                       89.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 90pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      English
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                                                                                                                                                       Score 1110;
Pred. No. 1
                                                                                                                                 Mismatches
                                                                                                                                     l.2e-96;
nes 0;
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                                                                                                                                                                       21;
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                                                                                                                                     Indels
                                                                                                                                                                     209;
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120
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ARCSULT 12
ARACITE 12

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  망
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 В
Matches
                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to novel soluble flt3 ligand (flt3-L) polypeptides which exhibits increased or decreased biological activity relative to the full length wild type (AAY69719) or mature (AAY69720) flt3-L polypeptides. This sequence represents an example of the novel flt-3 ligands and comprises the Q122R mutant polypeptide. The flt3-L protein binds cell surface tyrosine kinase receptors and regulate growth and differentiation of hematopoietic progenitor cells. The flt3-L protein be used to induce cellular expansion (especially in vivo) or dendritic cells, especially in the presence of growth factors such as interleukins,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Immunomodulator; immunosuppressive; cytostatic; antianemic; anti-HIV; neuroprotective; antiallergic; flt3 ligand; flt3-L; wild type; allergy; cell surface tyrosine kinase receptor; hematopoietic progenitor cell; cellular expansion; cellular differentiation; natural killer cell; cancer; dendritic cell; immune response; autoimmunity; immunosuppression; myelodysplasia; aplastic anemia; HIV infection; lymphoma; neuroblastoma; multiple myeloma; leukemia; mutein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Graddis TJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           02-JUL-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 05-JUL-2000
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                                                                                                                                                                                                              immunosuppression). The protein may be used to treat a pathological condition e.g. myelodysplasia, aplastic anemia, HIV infection, brea small cell lung, testicular or ovarian cancer, lymphoma, multiple
                                                                                                                                                                                                                                                                                                         modulate, augment or enhance a patient's immune response and can to treat an immune disorder (e.g. allergy, autoimmunity or
                                                                                                                                                                                                                                                                                                                                                                          colony stimulating factors or protein kinases. The protein can also
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mutant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2000-182115/16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25-JUN-1999;
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                                                                                                                       Sequence
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                             Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RQNFSRCLELQCQPDSSTLPPPWSPRPLEATAPTAPQPPLLLLLLLPVGLLLLAAAWCLH 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WQRTRRRTPRPGEQVPPVPSPQDLLLVEH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              soluble flt3 ligand polypeptide used in cellular expansion, response stimulation or treatment of pathological conditions as amino acid substitutions at positions 8, 84, 118 or 122 -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Page 88-89;
                                                                                                                                                                                        neuroblastoma
   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   McGrew JT;
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                             89.4%;
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Score 1110; D
Pred. No. 1.2e
1; Mismatches
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                                                                                                                                                                                           leukemia
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                         ; DB 21;
l.2e-96;
                                                             Length
   Indels
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                                                                                                                                                                                                                                                     breast,
Gaps
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27 TQDCSFQ\(\mathbf{x}\)SDFAVKIRELSDYLLQDYPVTVASNLQDEELCGGLWRLVLAQRWMERL 86

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RESULT 13
AAY69727
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                                                                              ligands and comprises the L26F mutant polypeptide. The flt3-L protein binds cell surface tyrosine kinase receptors and regulate growth and differentiation of hematopoletic progenitor cells. The flt3-L protein can be used to induce cellular expansion (especially in vivo) or differentiation, e.g. in hematopoletic, natural killer (NK) or dendritic cells, especially in the presence of growth factors such as interleukins, colony stimulating factors or protein kinases. The protein can also modulate agreement of the protein kinases.
                             modulate, augment or enhance a patient's immune response and can be to treat an immune disorder (e.g. allergy, autoimmunity or immunosuppression). The protein may be used to treat a pathological
                                                                                                                                                                                                                             The invention relates to novel soluble flt3 ligand (flt3-L) polypeptides which exhibits increased or decreased biological activity relative to the full length wild type (AAY69719) or mature (AAY69720) flt3-L
                                                                                                                                                                                                                                                                                                   Claim 13; Page 82-83;
                                                                                                                                                                                                                                                                                                                                     Mutant soluble flt3 ligand polypeptide used in cellular expansion, immune response stimulation or treatment of pathological condition contains amino acid substitutions at positions 8, 84, 118 or 122 \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cancer; dendritic cell; immune response; autoimmunity; immunosuppression;
myelodysplasia; aplastic anemia; HIV infection; lymphoma; neuroblastoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cell surface tyrosine kinase receptor; hematopoietic progenitor cell; cellular expansion; cellular differentiation; natural killer cell;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAY69727;
                                                                                                                                                                                         polypeptides. This sequence represents an example of the novel flt-3
ligands and comprises the L26F mutant polypeptide. The flt3-L protei
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Graddis TJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       02-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13-JAN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO200001823-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   multiple myeloma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         neuroprotective;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Immunomodulator;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human flt-3 mutein L26F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              05-JUL-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAY69727 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WQRTRRRTPRPGEQVPPVPSPQDLLLVEH 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WQRTRRRTPRPGEQVPPVPSPQDLLLVEH 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KTVAGSKMQGLLERVNTEIHFVTKCAFQPPPSCLRFVQTNISRLLQETSEQLVALKPWIT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KTVAGSKMQGLLERVNTEIHFVTKCAFQPPPSCLRFVQTNISRLLQETSEQLVALKPWIT 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RRNFSRCLELQCQPDSSTLPPPWSPRPLEATAPTAPQPPLLLLLLLPVGLLLLAAAWCLH
                                                                                                                                                                                                                                                                                                                                                                                                               2000-182115/16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IMMUNEX CORP
e.g. myelodysplasia, aplastic anemia, l lung, testicular or ovarian cancer,
                                                                                                                                                                                                                                                                                                                                                                                                                                                   McGrew JT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       98US-0109100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99WO-US14296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       immunosuppressive; cytostatic; antianemic; anti-HIV;
antiallergic; flt3 ligand; flt3-L; wild type; allergy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   leukemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Protein;
                                                                                                                                                                                                                                                                                                     90pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   mutein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ΑĀ
                    HIV infection,
                                                                                                                                                                                                                                                                                                                                            conditions
8 or 122 -
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RESULT 14
AAY69729
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Best Local
The invention relates to novel soluble flt3 ligand (flt3-L) polypeptides which exhibits increased or decreased biological activity relative to the full length wild type (AAY69719) or mature (AAY69720) flt3-L polypeptides. This sequence represents an example of the novel flt-3 ligands and comprises the L26F mutant polypeptide. The flt3-L protein binds cell surface tyrosine kinase receptors and regulate growth and differentiation of hematopoietic progenitor cells. The flt3-L protein car
                                                                                                                                  Mutant soluble flt3 ligand polypeptide used in cellular expansion, immune response stimulation or treatment of pathological conditions contains amino acid substitutions at positions 8, 84, 118 or 122 -
                                                                                                                     Claim 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                             cell surface tyrosine kinase receptor; hematopoietic progenitor cell; cellular expansion; cellular differentiation; natural killer cell; cancer; dendritic cell; immune response; autoimmunity; immunosuppression; myelodysplasia; aplastic anemia; HIV infection; lymphoma; neuroblastoma;
                                                                                                                                                                                                                                                        (IMMV ) IMMUNEX CORP
                                                                                                                                                                                                                                                                                    02-JUL-1998;
                                                                                                                                                                                                                                                                                                              25-JUN-1999;
                                                                                                                                                                                                                                                                                                                                         13-JAN-2000
                                                                                                                                                                                                                                                                                                                                                                     WO200001823-A2
                                                                                                                                                                                                                                                                                                                                                                                               Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                       multiple
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Immunomodulator; immunosuppressive; cytostatic; antianemic; anti-HIV; neuroprofective; antiallergic; flt3 ligand; flt3-L; wild type; allergy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        neuroprotective;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           05-JUL-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAY69729 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                             sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WQRTRRRTPRPGEQVPPVPSPQDLLLVEH 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RQNESRCLELQCQPDSSTLPPPWSPRPLEATAPTAPQPPLLLLLLLPVGLLLLAAAWCLH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KTVAGSKMQGLLERVNTEIHFVTKCAFQPPPSCLRFVQTNISRLLQETSEQLVALKPWIT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KTVAGSKMQGLLERVNTEIHFVTKCAFQPPPSCLRFVQTNISRLLQETSEQLVALKPWIT 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TQDCSFQHSPISSDFAVKIRELSDYFLQDYPVTVASNLQDEELCGGLWRLVLAQRWMERL
                                                                                                                                                                                                                              ΤJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                      myeloma;
                                                                                                                   Page
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           neuroblastoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 209
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                                                                                                                                                                                                                              McGrew
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                                                                                                                   78-79;
                                                                                                                                                                                                                                                                                    98US-0109100
                                                                                                                                                                                                                                                                                                            99WO-US14296
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                                                                                                                                                                                                                                                                                                                                                                                                                                    leukemia; mutein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Protein;
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                                                                                                             90pp;
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99.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          or
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                                                                                                                English.
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RESULT 15
AAY69722
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                        cell surface tyrosine kinase receptor; hematopoietic progenitor cell; cellular expansion; cellular differentiation; natural killer cell; cancer; dendritic cell; immune response; autoimmunity; immunosuppression; myelodysplasia; aplastic anemia; HIV infection; lymphoma; neuroblastoma;
                                                                                                                                                       02-JUL-1998;
                                                                                                                                                                                                                                            WO200001823-A2
                                                                                                                                                                                                                                                                         Synthetic
                                                                                                                                                                                                                                                                                                               multiple myeloma; leukemia; mutein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAY69722 standard; Protein;
                                                                                                                          (IMMV ) IMMUNEX CORP.
                                                                                                                                                                                    25-JUN-1999;
                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                         neuroprotective;
                                                                                                                                                                                                                                                                                                                                                                                                     Immunomodulator;
                                                                                                                                                                                                                                                                                                                                                                                                                                Human flt-3 mutein H8Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               05-JUL-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       condition e.g. myelodysplasia, apiastic a small cell lung, testicular or ovarian ca myeloma, neuroblastoma or acute leukemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     immunosuppression). The protein may be used to treat a pathological condition e.g. myelodysplasia, aplastic anemia, HIV infection, brea small cell lung, testicular or ovarian cancer, lymphoma, multiple
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               be used to induce cellular expansion (especially in vivo) or differentiation, e.g. in hematopoietic, natural killer (NK) or dendritic cells, especially in the presence of growth factors such as interleukins, colony stimulating factors or protein kinases. The protein can also modulate, augment or enhance a patient's immune response and can be used to treat an immune disorder (e.g. allergy, autoimmunity or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RQNFSRCLELQCQPDSSTLPPPWSPRPLEATAPTAPQPPLLLLLLLLPVGLLLLAAAWCLH
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                                                                                             McGrew
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                                                                                                                                                      98US-0109100.
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                                                                                                                                                                                                                                                                                                                                                                                immunosuppressive; cytostatic; antianemic; anti-HIV;
antiallergic; flt3 ligand; flt3-L; wild type; allergy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       89.4%;
99.5%;
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contains

Mutant soluble flt3 ligand polypeptide used in cellular expansion, immune response stimulation or treatment of pathological condition contains amino acid substitutions at positions 8, 84, 118 or 122

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Search completed: November 24, 2002, 10:10:12 Job time : 32.7704 secs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to novel soluble flt3 ligand (flt3-L) polypeptides cc which exhibits increased or decreased biological activity relative to cc the full length wild type (AAY69719) or mature (AAY69720) flt3-L. Cc polypeptides. This sequence represents an example of the novel flt-3 cc ligands and comprises the H8Y mutant polypeptide. The flt3-L protein comprises to induce expansion (especially in vivo) or dendritic comprises to induce cellular expansion (especially in vivo) or dendritic confirmation, e.g. in hematopoietic, natural killer (NK) or dendritic colls, especially in the presence of growth factors such as interleukins, cc colony stimulating factors or protein kinases. The protein can also condulate, augment or enhance a patient's immune response and can be used to treat an immune disorder (e.g. allergy, autoimmunity or condition e.g. myelodysplasia, aplastic anemia, HIV infection, breast, complete the protein may be used to treat a pathological condition e.g. myelodysplasia, aplastic anemia, HIV infection, breast, complete condition to the protein can be used to treat a pathological condition e.g. myelodysplasia, aplastic anemia, HIV infection, breast, condition to the protein can be used to treat a pathological condition e.g. myelodysplasia, aplastic anemia, HIV infection, breast, condition to the protein can be used to treat a pathological condition e.g. myelodysplasia, aplastic anemia, HIV infection, breast, condition to the protein can be used to treat a pathological condition e.g. myelodysplasia, aplastic anemia, HIV infection, breast, condition to the protein can be used to treat a pathological condition to the protein can be used to treat a pathological condition to the protein can be used to treat a pathological condition to the protein can be used to treat a pathological condition to the protein can be used to treat a pat
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Best Local Similarity 99.5%;
Matches 208; Conservative
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                                                                                                                                         181 WORTERETPREGEOVEPVESPODILLIVEH 209
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Pred. No. 1.9e-96;
1; Mismatches 0
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GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
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Database :	Post-processing:	Minimum DB seq Maximum DB seq	Total number	Searched:	Scoring table:	Title: Perfect score: Sequence:	Run on:	OM protein -
Published_Applications_AA:*  1: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*  2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*  3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*  4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*  5: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*  6: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*  7: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*  8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*  9: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*  10: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*  11: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*  12: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*  13: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep:*  14: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep:*	ng: Minimum Match 0% Maximum Match 100% Listing first 45 summaries	q length: 0 q length: 2000000000	Total number of hits satisfying chosen parameters: 100480	100480 seqs, 15661496 residues	: BLOSUM62 Gapop 10.0 , Gapext 0.5	US-09-448-378-1 : 1242 1 MTVLAPAMSPTTYLLLLLLLRPGEQVPPVPSPQDLLLVEH 235	November 24, 2002, 10:11:46 ; Search time 8.57296 Seconds (without alignments) 429.309 Million cell updates/sec	protein search, using sw model

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

17 18 19	13 14 15	7 10 11	165420	Result No.
768.5 768.5 506.5	1108 1107 1106 1100 768.5	1110 1110 1110 1110 1108	1242 1242 1242 1242 1242 1124 1124	Score
61.9 61.9 40.8	89.2 89.1 88.6	89.4 89.4 89.4	100.0 100.0 100.0 100.0 90.5 89.7	% Query Match Length
231 231 137	209 209 209 231	2009 2009 2009	235 235 235 235 212	
10 10	10 10 10	10 10 10	9 10 10 10	DB
US-09-448-378-2 US-09-983-806-2 US-09-904-536-19	US-09-904-536-15 US-09-904-536-13 US-09-904-536-16 US-09-904-536-16 US-10-095-449-2	US-09-904-536-9 US-09-904-536-12 US-09-904-536-17 US-09-904-536-17 US-09-904-536-11	US-10-095-449-6 US-09-448-378-1 US-09-983-806-6 US-09-904-536-1 US-09-904-536-18	SUMMARIES
Sequence 2, Appli Sequence 2, Appli Sequence 19, Appl	Sequence 15, Appl Sequence 13, Appl Sequence 8, Appli Sequence 16, Appl	14 11 11	Sequence 6, Appli Sequence 1, Appli Sequence 6, Appli Sequence 1, Appli Sequence 10, Appl	Description

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6.5	6.5	6.5	6.6	6.6	6.6	6.8	6.8	6.8	6.8	6.8	6.8	6.8	6.9	7.0	7.0	7.0	7.0	7.0	7.0	7.2	7.2	7.2	7.2	7.4	7.4
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US-10-047-542-45	US-09-916-230-1	US-10-047-542-60	US-09-957-995A-19	US-09-801-196-26	US-09-953-342-24	US-10-047-542-89	US-09-804-615-9	US-09-220-920-26	us-09-220-920-52	US-10-001-873-50	US-09-223-490-4	US-09-783-708-1	US-09-925-300-1680	US-09-874-923-104	US-09-991-496-104	US-10-108-605-57	US-09-935-727-8	US-09-907-372-20	US-09-826-212-6	US-09-211-755B-47	US-09-818-879-47	US-09-793-139-47	US-09-826-508-26	899-471	US-09-899-471-2
	e 1	60,		Sequence 26, Appl		Sequence 89, Appl	Sequence 9, Appli	26	Sequence 52, Appl	Sequence 50, Appl	Sequence 4, Appli	Sequence 1, Appli	168C	9 104	104,	Sequence 57, Appl	Sequence 8, Appli	20,	6,	•	e 47,	7	26		Sequence 2, Appli

## ALIGNMENTS

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NESULT 1
US-10-095-449-6
Sequence 6, Application US/10095449
Patent No. US20020150004A1

GENERAL INFORMATION:
APPLICANT: Lyman, Stewart D.
Beckmann, M. Patricia
TITLE OF INVENTION: Ligands for flt3/flk-2 Receptors
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSE: Stephen L. Malaska, Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: Washington
COUNTRY: US
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh
OPERATING SYSTEM: Macintosh
OPERATING SYSTEM: Macintosh
OPERATING SYSTEM: MSCONDOWN #5.1
APPLICATION NUMBER: US/10/095,449
FILING DATE: 13-Mar-2002
CLASSIFICATION NUMBER: US/10/95,449
FILING DATE: 13-Mar-2002
CLASSIFICATION NUMBER: US/869,692
FILING DATE: 13-Mar-2002
APPLICATION NUMBER: US/8616,407
FILING DATE: August 12, 1993
APPLICATION NUMBER: 08/66,692
FILING DATE: August 12, 1993
APPLICATION NUMBER: 08/16,463
FILING DATE: May 24, 1993
APPLICATION NUMBER: 08/106,463
APPLICATION NUMBER: 08/06,394
FILING DATE: May 24, 1993
APPLICATION NUMBER: 08/06,394
FILING DATE: May 24, 1993
APPLICATION NUMBER: 08/06,394
FILING DATE: May 24, 1993
APPLICATION NUMBER: 28/365
REPERENCE_DOCKET NUMBER: 28/365
FREERENCE_DOCKET NUMBER: 28/365
FREERENCE_DOCKET NUMBER: 28/365
FREERENCE_DOCKET NUMBER: 28/365
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TELEFAX:

(206)

233-0644

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RESULT 3
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US-09-448-378-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQ ID NO 1
LENGTH: 235
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Best Local Similarity
Matches 235; Conserv
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                            Matches
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CURRENT APPLICATION NUMBER: US/09/448,378
CURRENT FILING DATE: 1999-11-23
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PatentIn version 3.0
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TITLE OF INVENTION: Dendr
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TYPE: PRT
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INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
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                                                                APQPPLLLLLLPVGLLLLAAAWCLHWQRTRRRTPRPGEQVPPVPSPQDLLLVEH 235
                                                                               APQPPLLLLLLLPVGLLLLAAAWCLHWQRTRRRTPRPGEQVPPVPSPQDLLLVEH 235
                                                                                                                             RFVQTNISRLLQETSEQLVALKPWITRQNFSRCLELQCQPDSSTLPPPWSPRPLEATAPT
                                                                                                                                              RFVQTNISRLLQETSEQLVALKPWITRQNFSRCLELQCQPDSSTLPPPWSPRPLEATAPT
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Pred. No. 2e-103;
Mismatches 0
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Pred. No. 2e-103;
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                                                                                                                                                                                                                                                                                                                         Query Match
Best Local
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INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
181
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les 235; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear MOLECULE TYPE: protein SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Lyman, Stewart D.

Beckmann, M. Patricia
TITLE OF INVENTION: Ligands for flt3/flk-2 Receptors
                   APQPPLLLLLLLPVGLLLLAAAWCLHWQRTRRTTPRPGEQVPPVPSPQDLLLVEH 235
                                                                                                                                                                                                                        RFVQTNISRLLQETSEQLVALKPWITRQNFSRCLELQCQPDSSTLPPPWSPRPLEATAPT
                                                                                                                                                  ASNLQDEELCGGLWRLVLAQRWMERLKTVAGSKMQGLLERVNTEIHFVTKCAFQPPPSCL
                                                                                                                                                                      ASNLQDEELCGGLWRLVLAQRWMERLKTVAGSKMQGLLERVNTEIHFVTKCAFQPPPSCL
APQPPLLLLLLPVGLLLLAAAWCLHWQRTRRTPRPGEQVPPVPSPQDLLLVEH
                                                                       RFVQTNISRLLQETSEQLVALKPWITRQNFSRCLELQCQPDSSTLPPPWSPRPLEATAPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: 08/111,758
FILING DATE: August 25, 1993
APPLICATION NUMBER: 08/106,463
FILING DATE: August 12, 1993
APPLICATION NUMBER: 08/068,394
FILING DATE: May 24, 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 530
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/08/444,626
FILING DATE: 19-MAY-1995
APPLICATION NUMBER: US 08/162,407
FILING DATE: 03-DEC-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 235 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Malaska, Stephen L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 25-Oct-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: US
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                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                     100.0%; Score 1242; DB 1 100.0%; Pred. No. 2e-103;
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Street
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US-09-904-536-10
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US-09-904-536-10
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Best Local
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LENGTH: 212
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Patent No. US200201111475A1
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APPLICANT: McGrew, Jeffrey T.
TITLE OF INVENTION: FLI3-L MUTANTS AND METHODS OF
FILE REFERENCE: 03360.0028
CURRENT APPLICATION NUMBER: US/09/904,536
CURRENT FILING DATE: 2001-07-16
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Best Local Similarity
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CURRENT FILING DATE: 2001-07-16
PRIOR APPLICATION NUMBER: PRIOR APPLICATION: 09/109,100
PRIOR FILING DATE: 1999-07-02
NUMBER OF SEQ ID NOS: 20
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NUMBER OF SEQ ID NOS: 20
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APPLICANT: McGrew, Jeffrey T.
TITLE OF INVENTION: FLT3-L MUTANTS AND METHODS OF
FILE REFERENCE: 03260.0028
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TYPE: PRT
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                 RLKTVAGSKMQGLLERVNTEIHFVTKCAFQPPPSCLRFVQTNISRLLQETSEQLVALKFW 144
                                                             RFVQTNISRLLQETSEQLVALKPWITRQNFSRCLELQCQPDSSTLPPPWSPRPLEATAPT
RLKTVAGSKMQGLLERVNTEIHFVTKCAFQPPPSCLRFVQTNISRLLQETSEQLVALKPW
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; Pred. No. 5.4e-93;
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Pred. No. 2e-103;
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-904-536-9
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APPLICANT: Graddis, Thomas J.
APPLICANT: MCGrew, Jeffrey T.
TITLE OF INVENTION: FLT3-L MUTANTS AND METHODS
FILE REFERENCE: 03260.0028
                                                                SOFTWARE: PatentIn Ver. 2.1 SEQ ID NO 9
                                                                                                                                                                                                                                                                     Sequence 9, Application US/09904536 Patent No. US20020111475A1
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                                                                                               PRIOR APPLICATION NUMBER: PRIOR APPLICATION: 09/109,100 PRIOR FILING DATE: 1999-07-02 NUMBER OF SEQ ID NOS: 20
                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/904,536 CURRENT FILING DATE: 2001-07-16
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APPLICANT: McGrew, Jeffrey T.
TITLE OF INVENTION: FLT3-L MUTANTS AND METHODS OF USE
FILE REFERENCE: 03260.0028
CURRENT APPLICATION NUMBER: US/09/904,536
CURRENT FILING DATE: 2001-07-16
PRIOR APPLICATION NUMBER: PRIOR APPLICATION: 09/109,100
PRIOR FILING DATE: 1999-07-02
NUMBER OF SEQ ID NOS: 20
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ORGANISM: Homo sapiens
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TYPE: PRT
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es 209; Conserv
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Pred. No. 4.1e-92;
0; Mismatches 0;
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Matches 208
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SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 12
LENGIH: 209
GENERAL INFORMATION:
APPLICANT: Graddis, Thomas J.
APPLICANT: Graddis, Thomas J.
APPLICANT: MCGREW, Jeffrey T.
TITLE OF INVENTION: FLT3-L MUTANTS AND METHODS
FILE GEFERENCE: 03260.0028
CURREN APPLICATION NUMBER: US/09/904,536
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Patent No. US200201111475A1
                                                                                                Sequence 14, Application US/09904536 Patent No. US200201111475A1
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APPLICANT: McGrew, Jeffrey T.
APPLICANT: McGrew, Jeffrey T.
ITLE OF INVENTION: FLT3-L MUTANTS AND METHODS OF USE
FILE REFERENCE: 03260.0028
CURRENT APPLICATION NUMBER: US/09/904,536
CURRENT FILING DATE: 2001-07-16
PRIOR APPLICATION NUMBER: PRIOR APPLICATION: 09/109,100
PRIOR FILING DATE: 1999-07-02
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Pred. No. 9.3e-92;
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Pred., No. 9.3e-92;
0; Mismatches 1;
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US-09-904-536-17
Sequence 17, Application US/09904536
Patent No. US20020111475A1
GENERAL INFORMATION:
APPLICANT: Graddis, Thomas J.
APPLICANT: McGrew, Jeffrey T.
TITLE OF INVENTION: FLT3-L MUTANTS AND
FILE REFERENCE: 03260.0028
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Best Local Similarity
Matches 208; Conserv
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Best Local :
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PRIOR APPLICATION NUMBER: PRIOR /
PRIOR FILING DATE: 1999-07-02
NUMBER OF SEQ ID NOS: 20
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CURRENT FILING DATE: 2001-07-16
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TYPE: PRT
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TYPE: PRT
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Pred. No. 9
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Pred. No. 9.3e-92;
1; Mismatches 0
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APPLICANT: Graddis, Thomas J.
APPLICANT: McGrew, Jeffrey T.
APPLICANT: McGrew, Jeffrey T.
APPLICANT: McGrew, Jeffrey T.
TITLE OF INVENTION: ELT3-L MUTANTS AND METHODS OF USE
FILE REFERENCE: 03260.0028
CURRENT APPLICATION NUMBER: US/09/904,536
CURRENT FILING DATE: 2001-07-16
PRIOR APPLICATION NUMBER: PRIOR APPLICATION: 09/109,100
PRIOR EILING DATE: 1999-07-02
NUMBER OF SEQ ID NOS: 20
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 11
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                                                                                                                                                                                                                                                             Query Match
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APPLICANT: McGrew, Jeffrey T.
APPLICANT: McGrew, Jeffrey T.
TITLE OF INVENTION: FLT3-L MUTANTS AND METHODS OF USE
FILE REFERENCE: 03260.0028
CURRENT APPLICATION NUMBER: US/09/904,536
CURRENT FILING DATE: 2001-07-16
PRIOR APPLICATION NUMBER: PRIOR APPLICATION: 09/109,100
PRIOR FILING DATE: 1999-07-02
NUMBER OF SEQ ID NOS: 20
CONTRACTOR OF THE OWNER OWNER OF THE OWNER 
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Pred. No. 1.4e-91;
1; Mismatches 0;
                                                                                                                                                                                                                                 Pred. No.
                                                                                                                                                                                                                                                             Score 1108; DB 10;
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                                                                                                                                                                                                                                    Sequence 8, Application US/09904536 Patent No. US20020111475A1 GENERAL INFORMATION:
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                            SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 8
LENGTH: 209
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Best Local (
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APPLICANT: McGrew, Jeffrey T.
APPLICANT: McGrew, Jeffrey T.
TITLE OF INVENTION: FLT3-L MUTANTS AND METHODS OF USE
FILE REFERENCE: 03260.0028
CURRENT APPLICATION NUMBER: US/09/904,536
CURRENT FILING DATE: 2001-07-16
PRIOR APPLICATION NUMBER: PRIOR APPLICATION: 09/109,100
PRIOR APPLICATION NUMBER: PROPOSED OF SEQ ID NOS: 20
NUMBER OF SEQ ID NOS: 20
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APPLICANT: McGrew, Jeffrey T.
TITLE OF INVENTION: F1T3-L MUTANTS AND METHODS
FILE REFERENCE: 03260.0028
                                                                               PRIOR APPLICATION NUMBER: PRIOR APPLICATION: 09/109,100 PRIOR FILING DATE: 1999-07-02 NUMBER OF SEQ ID NOS: 20
                                                                                                                                  CURRENT APPLICATION NUMBER: US/09/904,536 CURRENT FILING DATE: 2001-07-16
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ORGANISM: Homo sapiens
ORGANISM: Homo sapiens
                  TYPE: PRT
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PRIOR APPLICATION NUMBER: PRIOR APPLICATION: 09/109,100
PRIOR FILING DATE: 1999-07-02
NUMBER OF SEQ ID NOS: 20
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 16
LENGTH: 209
TYPE: PRT
ORGANISM: Homo sapiens
US-09-904-536-16
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; Sequence 16, Application US/09904536
; Patent No. US20020111475A1
; GENERAL INFORMATION:
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Best Local Similarity 99.5%;
Matches 208; Conservative
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APPLICANT: McGrew, Jeffrey T.
TITLE OF INVENTION: FLT3-L MUTANTS AND METHODS
FILE REFERENCE: 03260.0028
CURRENT APPLICATION NUMBER: US/09/904,536
CURRENT FILING DATE: 2001-07-16
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